



SEQUENCE LISTING #3

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<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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<140> 09/665,350

<141> 2000-09-18

<150> PCT/US00/04414

<151> 2000-02-22

<150> US 60/143,048

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<150> US 60/145,698

<151> 1999-07-26

<150> US 60/146,222

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<212> PRT
<213> Homo sapiens

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20 25 30

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
35 40 45

Ala Lys Lys Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
50 55 60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
65 70 75 80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
85 90 95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
100 105 110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
115 120 125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
130 135 140

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
 245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
260 265 270

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
290 295 300

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Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
340 345 350

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<211> 2206
<212> DNA
<213> *Homo sapiens*

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<211> 379
<212> PRT
<213> *Homo sapiens*

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
145 150 155 160

Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
165 170 175

Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
180 185 190

Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
195 200 205

Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
210 215 220

Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
225 230 235 240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
245 250 255

Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
260 265 270

Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
275 280 285

Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
290 295 300

Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
305 310 315 320

His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
325 330 335

Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
340 345 350

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
370 375

<210> 5
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 5
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<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 6
agagtgtatc tctggctacg c

21

<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 7
taagtccggc acattacagg tc

22

<210> 8
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 8
cccacgatgt atgaatggtg gactttgtgt gactcctggc ttctgcattc

49

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 9
aaagacgcat ctgcgagttt cc

22

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 10
tgctgatttc acactgtct ccc

23

<210> 11
<211> 2197
<212> DNA

<213> *Homo sapiens*

<400> 11

<210> 12

<211> 164

<212> PRT

<213> *Homo sapiens*

<400> 12

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His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
20 25 30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu

50	55	60
Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr		
65	70	75
Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro		
85	90	95
Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr		
100	105	110
Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln		
115	120	125
Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln		
130	135	140
Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly		
145	150	155
His Asp Pro Gly		

<210> 13
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 <212> DNA
 <213> Homo sapiens

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 <222> (33)..(33)
 <223> a, t, c or g

<220>
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 <222> (37)..(37)
 <223> a, t, c or g

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 <223> a, t, c or g

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 <222> (144)..(144)
 <223> a, t, c or g

<220>
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 <222> (188)..(188)
 <223> a, t, c or g

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<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 14
ttcgaggcct ctgagaagtg gccc 24

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 15
ggcggttatct ctctggcctc cc 22

<210> 16
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 16
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<210> 17
<211> 960
<212> DNA
<213> Homo sapiens

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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

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Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
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Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
180 185

<210> 19

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 19
tgctgtgcta ctccctgcaaa gccc 24

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 20
tgcacaaggc ggtgtcacag cacg 24

<210> 21
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 21
agcaacgagg actgcctgca ggtggagaac tgcacccagg tggg 44

<210> 22
<211> 1200
<212> DNA
<213> Homo sapiens

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
195 200 205

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 24
cagtacgta gggaccaggg cgccatga 28

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 25
ccggtgacct gcacgtgctt gccaa 24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<220>
<221> modified_base
<222> (21)..(21)
<223> a, t, c or g

<400> 26
gcggatctgc cgcctgctca nctggtcggt catggcgccc t 41

<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 27
acttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60
aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120
ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
tccagtcatt ttgattttgc tggttatttt ttttttctt ttcttttcc caccacattg 240
tattttattt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300
ctttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360
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gggccttccg ggaggctatt agcctcaaattt tggtgtttt gtctaagaat cacctgagca 780
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gcattaatta cacagactgc catatccccca acaacatgcg atactgcaac agcagcgtgc 2220
cagacctgga gcactgccc acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280
tagactctt agaacacact cgtgtgtca cataaagaca cgcagattac atttgataaa 2340
tgttacacag atgcatttgc gcatttgaat actctgtaat ttatacgggt tactatataa 2400
tgggatttaa aaaaagtgc atctttcta tttcaagtta attacaaca gttttgtaac 2460
tcttgcttt ttaaatctt 2479

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
1 5 10 15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser

130 135 140
Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
145 150 155 160
Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
165 170 175
Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
180 185 190
Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
195 200 205
Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
210 215 220
Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
225 230 235 240
Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
245 250 255
Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
260 265 270
Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
275 280 285
Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
290 295 300
Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
305 310 315 320
Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
325 330 335
Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
340 345 350
Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro
355 360 365
Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
370 375 380
Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
385 390 395 400
Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg
405 410 415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val
420 425 430
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met

435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
560		
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
640		
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
660		

<210> 29
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 29
 cggtctacct gtatggcaac c

<210> 30

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 30
gcaggacaac cagataaacc ac 22

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 31
acgcagattt gagaaggctg tc 22

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 32
ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac 46

<210> 33
<211> 3449
<212> DNA
<213> Homo sapiens

<400> 33
actggagca agcggcggcg gcgagacag aggcagaggc agaagctggg gctccgtcct 60
cgctccac gagcgatccc cgaggagagg cgccggccctc ggcgaggcga agaggccgac 120
gagaagacc cgggtggctg cggccctgcc tcgcctccca ggccggcg gctgcagcct 180
tgccctt gctcgctt aaaaatggaaa agatgctcgc aggctgcattt ctgctgatcc 240
tcggacagat cgtcctccctc cctgcccggg ccaggagcg gtcacgtggg aggtccatct 300
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 ctgttagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatataat 3360
 gtatatggat gtatgcataa aatcatagga catatgtact tttgtggaaacaa gttggatttt 3420
 ttatataataa ttaaaattca ccacttcag 3449

<210> 34
 <211> 915
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
 1 5 10 15
 Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
 20 25 30
 Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His
225 230 235 240

Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
245 250 255

Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser
260 265 270

Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His
275 280 285

Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln
290 295 300

Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala
305 310 315 320

Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val
325 330 335

Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu
340 345 350

Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn
355 360 365

Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr
370 375 380

Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys
385 390 395 400

Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu
405 410 415

Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe
420 425 430

Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu
435 440 445

Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser
450 455 460

Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys
465 470 475 480

Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu
485 490 495

His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu
500 505 510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
515 520 525

Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
530 535 540

Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
545 550 555 560

Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
565 570 575

Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
580 585 590

Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
595 600 605

Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
610 615 620

Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
625 630 635 640

Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
690 695 700

Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
705 710 715 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
725 730 735

Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
740 745 750

Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
770 775 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
900 905 910

Arg Tyr Arg
915

<210> 35
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 35
 gtgaccctgg ttgtgaatac tcc 23

<210> 36
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 36
 acagccatgg tctatagctt gg 22

<210> 37
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 37
 gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45

<210> 38
 <211> 1813
 <212> DNA
 <213> Homo sapiens

<400> 38
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 cggcacctgc aggtccgtgc gtccccggc tggcgccccct gactccgtcc cggccaggga 120
 gggccatgtat ttccctcccg gggcccccgg tgaccaactt gctgcggtt ttgttcctgg 180
 ggctgagtgc cctcgcgccc ccctcgcggg cccagctgca actgcacttg cccgccaacc 240
 ggttgcaggc ggtggagggaa gggaaagtgg tgcttccagc gtggtaacacc ttgcacgggg 300
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<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

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Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
20 25 30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
35 40 45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
50 55 60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
65 70 75 80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
85 90 95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
100 105 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val
115 120 125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
130 135 140

Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
145 150 155 160

Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
165 170 175

Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
180 185 190

Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
195 200 205

Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
210 215 220

Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
225 230 235 240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
245 250 255

Thr Leu Val Gly Leu Gly Leu Ala Gly Leu Val Leu Leu Tyr His
260 265 270

Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
275 280 285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
370 375 380

Gln Ala Gly Ser Leu Val
385 390

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 40
agggtctcca ggagaaagac tc 22

<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 41	
attgtgggcc ttgcagacat agac	24
<210> 42	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 42	
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc	50
<210> 43	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 43	
gtgtgacaca gcgtggc	18
<210> 44	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 44	
gaccggcagg cttctgcg	18
<210> 45	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 45	
cagcagcttc agccaccagg agtgg	25
<210> 46	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 46

ctgagccgtg ggctgcagtc tcgc

24

<210> 47

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 47

ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc

45

<210> 48

<211> 2822

<212> DNA

<213> Homo sapiens

<400> 48

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aa 2822

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
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Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
20 25 30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
35 40 45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
100 105 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
130 135 140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
145 150 155 160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
165 170 175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr
180 185 190

Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val
195 200 205

Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys
210 215 220

Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe
225 230 235 240

Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys
245 250 255

Val Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met
260 265 270

Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala
275 280 285

Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser
290 295 300

Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln
305 310 315 320

Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile
325 330 335

Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys
340 345 350

Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser
355 360 365

Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp
370 375 380

Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser
385 390 395 400

Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly
405 410 415

Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln
420 425 430

Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr
435 440 445

Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys
450 455 460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
675 680 685

Leu Arg
690

<210> 50
<211> 589
<212> DNA
<213> Homo sapiens

<220>
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<222> (61)..(61)
<223> a, t, c or g

<400> 50

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gtatttgtcc ctttgcttc atcatctgac aacttcttat tgaaacctca aaattatgtat 180
aattctgaag aggagggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccacccacat tatatgaact tgaaaaata acatttacat taagtcatcg aaaggtcaca 300
gataggtata ggagtctatg tggcattttg gaataactcac ctgataccat gaatggcagc 360

tggcttcag agggctgtga gctgacatac tcaaattgaga cccacaccc 420
aatcacctga cacatttgc aattttgatg tcctctggc cttccattgg tattaaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta tttcaactgat ttgtcttgcc 540
atatgcatt ttaccttctg gttttcagt gaaattcaaa gcaccagga 589

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 51
ggtaatgagc tccattacag 20

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 52
ggagtagaaa gcgcattgg 18

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 53
cacctgatac catgaatggc ag 22

<210> 54
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 54
cgagctcgaa ttaattcg 18

<210> 55
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 55
 ggatctcctg agtcagg

18

<210> 56
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 56
 cctagtttag ttagtccttgc aag

23

<210> 57
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 57
 atgagaccca cacctcatgc cgctgtatcc acctgacaca ttttgcatt

50

<210> 58
 <211> 2137
 <212> DNA
 <213> Homo sapiens

<400> 58
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gaggtttgtt ttgtatatta aaatggagtt tgtttgtt 2137

<210> 59
<211> 216
<212> PRT
<213> Homo sapiens

<400> 59
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
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His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
35 40 45
Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
50 55 60
Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
65 70 75 80
Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
85 90 95
Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
100 105 110
Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Ile Arg Pro
115 120 125
Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
130 135 140
Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
145 150 155 160
Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
210 215

<210> 60
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 60
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<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 61
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<210> 62
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 62
ccagtccggc gacaagccca aa 22

<210> 63
<211> 1295
<212> DNA
<213> Homo sapiens

<400> 63
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ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360

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tagtgccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tgaaagtatt 480
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tggcatccgt ttgctagaaa atcccgact tggctccaa agcaccaaca gctcatacac 660
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gctcacgcct gtaatcccag cactttggaa ggccgcggcg ggcggatcac gaggtcagga 1020
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ctggcatgg tggcatgtgc ctgcagttcc agtgcgttg gagacaggag aatcaactga 1140
accggggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcga gcctggtaa 1200
cagagcaaga ttccatctca aaaaataaaa taaaataata aataaataact gtttttacc 1260
tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64

<211> 312

<212> PRT

<213> Homo sapiens

<400> 64

Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr
1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
35 40 45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
50 55 60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
65 70 75 80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
85 90 95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
100 105 110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
115 120 125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
130 135 140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
145 150 155 160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
165 170 175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met

180	185	190
Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp		
195	200	205
Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg		
210	215	220
Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile		
225	230	235
Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu		
245	250	255
Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser		
260	265	270
Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn		
275	280	285
Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala		
290	295	300
Gly Gly Ser Arg Gly Gln Glu Phe		
305	310	

<210> 65

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 65

atcgttgtga agtttagtgcc cc

22

<210> 66

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 66

acctgcgata tccaaacagaa ttg

23

<210> 67

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 67
ggaagaggat acagtcactc tggaaagtatt agtggctcca gcagttcc 48

<210> 68
<211> 2639
<212> DNA
<213> Homo sapiens

<400> 68
gacatcgag gtgggcttagc actgaaactg ctttcaaga cgaggaagag gaggagaaag 60
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gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata tttacttct 180
aaataaatga attactcaat ctccatgac catctataca tactccacct tcaaaaagta 240
catcaatatt atatcattaa gggaaatagta accttctt ctccaatatg catgacattt 300
ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgggttcta 360
tggcattcat catttgacaa atgcaagcat cttccttatac aatcagctcc tattgaactt 420
actagcactg actgtggaat ccttaaggc ccattacatt tctgaagaag aaagctaaga 480
tgaaggacat gccactccga attcatgtgc tacttgcct agctatcact acactagtac 540
aagctgtaga taaaaaaatgt gattgtccac ggttatgtac gtgtgaaatc aggccttgg 600
ttacacccag atccatttat atggaagcat ctacagtggta ttgtaatgat ttaggtctt 660
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tcttttttca cgataacagg cttattaaag taccatgt tgctcttcaa aaagttgtaa 1260
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ccttcactg tagagctact gcagaaccac agcctgaaat ctactggata acacccctcg 1860
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tagatataaa tggcgtaact cccaaagaag ggggttata tacttgtata gcaactaacc 1980
tagttggcgc tgacttgaag tctgttatga tcaaagtggta tggatctttt ccacaagata 2040
acaatggctc ttgtatattt aaaaataagag atattcaggc caattcaggta ttgggtgtcct 2100
ggaaagcaag ttctaaaattt ctcataatcta gtgtttaatg gacgcctt gtcaagactg 2160
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ctcatctgaa tccatcaact gaggataaaaa tttgtattga tattccaccatctatcaga 2280
aaaacagaaaaaaa aatgtgtaa aatgtcacca ccaaagggtt gcacccctgtat caaaaagagt 2340
atggaaaagaa taataccaca acacttatgg cctgtttgg aggcccttctg gggattattg 2400
gtgtgatatg tcttacatcg tgcctctc cagaaatgaa ctgtgtgggt ggacacacgt 2460
atgtgaggaa ttacttacag aaaccaaccc ttgcatttagg tgagctttat ctcctctga 2520
taaatctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580
taggttacc aacaaatatg tcctaaaaac caccaaggaa acctactccaa aaaaatgaac 2639

<210> 69

<211> 708
<212> PRT
<213> Homo sapiens

<400> 69
Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
1 5 10 15
Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
20 25 30
Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
35 40 45
Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
50 55 60
Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Gln Thr Asn Asn
65 70 75 80
Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
85 90 95
Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
100 105 110
Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
115 120 125
Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
130 135 140
Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
145 150 155 160
Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
165 170 175
Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
180 185 190
Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
195 200 205
Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
210 215 220
Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
225 230 235 240
Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
245 250 255
Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
260 265 270
Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu

275	280	285
Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala		
290	295	300
Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro		
305	310	320
Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu		
325	330	335
Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly		
340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	480
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	560
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		

580

585

590

Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn
595 600 605

Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn
610 615 620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

gcccggact ggcgcaaggt gcccaagcaa ggaaagaaaat aatgaagaga cacatgtgtt 60
agctgcagcc ttttgaaaaca cgcaagaagg aaatcaatag tggacagg gctggacact 120
ttaccacgtct tggaggtat gatgaggaat gggctcgtga ttatgctgac attccagcat 180
gaatctggta gacctgtgtt taaccgttc cctctccatg tgcctcctcc tacaaagttt 240
tgccttatg atactgtgct ttcattctgc cagttatgtt cccaaagggtt gtctttgttc 300
ttccctctggg gtttaaatg tcacctgttag caatgaaat ctcaaggaaa taccttagaga 360
tctccctcct gaaacagtct tactgtatct ggactccaaat cagatcacat ctattccaa 420
tgaaatttt aaggacctcc atcaacttgat agttctcaac ctgtccaaaa atggcattga 480
gttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttg 540
cgacaatcggtt attcaaagtgc tgacaaaaaa tgccttcaat aacctgaaagg ccaggccag 600
aattgccaac aaccctggc actgcgactg tactctacag caagttctga ggagcatggc 660
gtccaatcat gagacagccc acaacgtat ctgtaaaaacg tccgtgttg atgaacatgc 720
tggcagacca ttccctcaatg ctgccaacga cgctgaccc ttgtaacctcc ctaaaaaaaac 780
taccgattat gccatgtgg tcaccatgtt tggctggttc actatggtga tctcatatgt 840
ggtatattat gtgaggcaaa atcaggagga tgccggaga cacctcgaaat acttggaaatc 900
cctgccaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatgt 960
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ggtttacttc tcccatccat tgaaacatt tgaaactttt tatttcaggat tttttgaat 1080
tatgccactg ctgaactttt aacaaacact acaacataaa taatttgagt ttaggtgatc 1140
cacccttaa ttgtacccccc gatggatata ttctgagtaa gctactatct gaacatttagt 1200
tagatccatc tcactatcta ataatgaaat ttatttttt aattaaaag caaataaaag 1260
cttaactttg aaccatggaa aaaaaaaaaaa aaaaaaaaaaa aaaca 1305

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu
1 5 10 15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
245 250 255

Thr Val Val .

<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

accgagccga gcggaccgaa ggccgcggcc agatgcaggt gagcaagagg atgctggcgg 60
gggcgttag gacatgccc agcccccctcc tggcctgctg gcagcccatc ctcctgctgg 120
tgctggctc agtgcgttca ggctcgccca cgggctgccc gccccgctgc gagtgcgtccg 180
cccaggaccg cgctgtgctg tgccaccgca agtgcgttgc ggcagtcggc gagggcatcc 240
ccaccgagac gcgcctgctg gacccaggca agaaccgcat caaaacgctc aaccaggacg 300
atgcgcagg cttccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tggagcccg cgccttcaac aaccttca acctccggac gtcgggtctc cgcagcaacc 420
gcctgaagct catcccgcta ggcgttca ctggccttag caacctgacc aagcaggaca 480
tcagcgagaa caagatcgaa atcctactgg actacatgtt tcaggacatc tacaacatca 540
atgcactgga gttggcgac aatgacatcg tctacatctc tcaccgcgg ttcagcgcc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacatc gacccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgatc tgaggctccg gcacctcaac atcaatgcca 720
tccgggacta ctccctcaag aggctgtacc gactcaaggt cttggagatc tcccactggc 780
cctacttggc caccatgaca cccaaactgccc tctacggcc caacctgacc tccctgtcca 840
tcacacactg caatctgacc gctgtgcctt acctggccgt cggccaccta gtctatctcc 900
gcttcctcaa ccttcctac aacccatca gcaccattga gggctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctgggtt gcccggcagct ggccgtggg gggccctatg 1020
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tggaggaatc agtcttccac tcgggtggca acctggagac actcatctg gactccaacc 1140
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accggcagca gcccacgtgc gccacgccc agttgtcca gggcaaggag ttcaaggact 1260
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aggcccagca ggtgtttgtt gacgagggcc acacgggtca gtttgtgtc cggggccatg 1380
gcgaccggcc gcccgcatac ctctggctt caccggaaa gcacctggc tcagccaaga 1440
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cccacctgca tgcgcgcagc tactcgccc actggccca tcagcccaac aagacatcg 1620
cttcatctc caaccagccg ggcgagggag aggccaaacag caccgcgc actgtgcctt 1680
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agcacaacat cgagatcgat tatgtgcccc gaaagtcgaa cgcaggatc agctccggc 1860
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cgggcgcccg ggcagggaa gggcctggg cgcacactgc tcactctcca gtccttccca 1980
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ggaccccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
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aaaaaaaaaa 2290

<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
1 5 10 15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
20 25 30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys

35	40	45
Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala		
50	55	60
Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys		
65	70	75
80		
Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His		
85	90	95
Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro		
100	105	110
Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser		
115	120	125
Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn		
130	135	140
Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp		
145	150	155
160		
Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp		
165	170	175
Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser		
180	185	190
Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr		
195	200	205
Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His		
210	215	220
Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg		
225	230	235
240		
Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr		
245	250	255
Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His		
260	265	270
Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr		
275	280	285
Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly		
290	295	300
Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly		
305	310	315
320		
Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr		
325	330	335
Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu		

340

345

350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
355 360 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
435 440 445

Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn
580 585 590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser
595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile
610 615 620

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 74
tcacacctggag cctttattgg cc 22

<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 75
ataccaggcta taaccaggct gcg 23

<210> 76
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 76
caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg 50
gg 52

<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 77
ccatgtgtct cctcctacaa ag 22

<210> 78
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 78
ggaaatagat gtgatctgat tgg 23

<210> 79
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 79
cacctgttagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50

<210> 80
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 80
agcaaccgccc tgaagctcat cc 22

<210> 81
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 81
aaggcgcggt gaaagatgta gacg 24

<210> 82
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 82
gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 83
cccacgcgtc cgcacacctgg cccccgggctc cgaagcggct cggggggcgcc ctttcggta 60
acatcgtagt ccacccccc cccatccccca gccccccgggg attcaggctc gccagcgccc 120
agccaggaggag ccggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180

tcctgctgtt cgcctgctgc tggcgcccg gcggggccaa cctctccag gacgacagcc 240
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 tgaaagatca cgaggactca tccctgcaat ggtctaacc cgtctac 360
 ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420
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 cccttccgt ggcttctctg catttgggtt attattattt ttgttaacaat cccaaatcaa 1620
 atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1680
 aaaca 1685

<210> 84

<211> 398

<212> PRT

<213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala
 1 5 10 15

Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
 20 25 30

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
385 390 395

<210> 85
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 85
gcttaggaatt ccacagaagc cc 22

<210> 86
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 86
aacctggaat gtcaccgagc tg 22

<210> 87
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 87
cctagcacag tgacgaggga cttggc 26

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 88
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 89
gcctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
<211> 2755
<212> DNA

<213> Homo sapiens

<400> 90

gggggttagg gaggaaggaa tccaccccca ccccccaaa ccctttctt ctcccttcct 60
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gctgttactt tgtatgaga tcgggatga attgctcgct taaaaatgc tgcttggat 180
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

Met Leu Leu Trp Ile Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala

1 5 10 15

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
115 120 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
180 185 190

Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
195 200 205

Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
210 215 220

Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
225 230 235 240

Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
245 250 255

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
260 265 270

Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
275 280 285

Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
290 295 300

Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg

305	310	315	320
Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala			
325		330	335
Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly			
340	345		350
Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala			
355	360	365	
Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp			
370	375	380	
Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn			
385	390	395	400
Leu Ile Leu Leu Asp Leu Gly Asn Asn Ile Ala Thr Val Glu Asn			
405	410		415
Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser			
420	425	430	
Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn			
435	440	445	
Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro			
450	455	460	
Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn			
465	470	475	480
Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu			
485	490	495	
Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala			
500	505	510	
Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly			
515	520	525	
Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala			
530	535	540	
Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr			
545	550	555	560
Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu			
565	570	575	
Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His			
580	585	590	
Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser			
595	600	605	
Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu			

610 615 620
Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
625 630 635 640

Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
645 650 655

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr
660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp
675 680 685

Cys Gly Ser His Ser Leu Ser Asp
690 695

<210> 92
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 92
gttggatctg ggcaacaata ac 22

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 93
attgttgtgc aggctgagtt taag 24

<210> 94
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 94
ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95
<211> 2226
<212> DNA
<213> Homo sapiens

<400> 95

agtcgactgc gtccccgtta cccggcgcca gctgtgttcc tgaccccaga ataactcagg 60
gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgccgcctaa gggaaactgt 120
tggccgctgg gccccggggg ggattcttgg cagttggggg gtccgtcggg agcgaggcg 180
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gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
1 5 10 15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val

50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
65 70 75 80

Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
85 90 95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
305 310 315 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln
340 345 350

Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala

355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	

<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 97
tggaaggaga tgcgatgcca cctg 24

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 98
tgaccagtgg ggaaggacag 20

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 99
acagagcaga ggggccttg 20

<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 100
tcagggacaa gtgggtctc tccc 24

<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 101
tcagggagg agtgtgcagt tctg 24

<210> 102
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 102
acagctcccg atctcagttt cttgcattcg 50

<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens

<400> 103
cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagtcctca gggaaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgcctt gccggccgcg 120
tatccccccgg ctacctggc cggcccgccgg cggtgccgcgt gtgagaggga ggcgcgggc 180
agccgagcgc cggtgtgagc cagcgctgct gccagtgtga gcggcggtgt gagcgcgggtg 240
ggtgccggagg ggcgtgtgtg cccgcgcgcg cggccgtgggg tgcaaaccggc gagcgtctac 300
gctgccatga ggggcgcgaa cgcctggcgc ccactctgc tgctgctggc tgccgccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgtttca catgtgttgg cattttact 420
ggagagtctg gatttattgg cagtgaagggt tttcctggag tgcaccctcc aaatagcaaa 480
tgtacttgaa aaatcacagt tcccgaagga aaagttagtcg ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgcccgtat gactttgtgg atgtgtacaa tggccatgcc 600

aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgggtccagt 660
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ctaaaagtgt caagcgttga cagcttggaa gcgttattt atacatctt gtaaaaggat 1860
attttagaat tgagttgtgtt gaagatgtca aaaaaagatt tttagaagtgc aatatttata 1920
gtgttatttg ttccaccccttc aagccttgc cctgaggtgt tacaatcttgc tcttcgtt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaaa 2026

<210> 104
<211> 415
<212> PRT
<213> Homo sapiens

<400> 104
Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
260 265 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala
340 345 350

Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro
355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu
370 375 380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys
385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys
405 410 415

<210> 105
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105
ccgattcata gacctcgaga gt 22

<210> 106
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106
gtcaaggagt cctccacaat ac 22

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107
gtgtacaatg gccatccaa tggccagcgc attggccgct tctgt 45

<210> 108
<211> 1838
<212> DNA
<213> Homo sapiens

<400> 108
cggacgcgtg ggcggacgcg tggcgcccc acggcgccc cgggctgggg cggtcgcttc 60
ttccttctcc gtggcctacg agggtccccca gcctggtaa agatggcccc atggccccc 120
aaggccctag tcccagctgt gctctggggc ctcagccctt tcctcaaccc cccaggaccc 180
atctggctcc agccctctcc acctcccccag tcttctcccc cgcctcagcc ccatccgtgt 240
catacctgcc ggggactggt tgacagctt aacaaggccc tggagagaac catccggac 300
aactttggag gtggaaacac tgcctggag gaagagaatt tgccttcaata caaagacagt 360
gagaccgcgc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgcac 420
cgccctgctgg agctgagtga ggagctggg gagagctggt ggtttcacaa gcagcaggag 480
gccccggacc tcttccagtg gctgtgctca gattccctga agctctgctg ccccgccaggc 540
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tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgccc 720
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cagatcccttccag agtcagcagg cttcttcata gagatgacag aagacgagtt ggtggcgtg 1200

cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taagggcgac 1260
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gagcgcagt accgtgtgct ggagggcttc atcaaggca gataatcgcg gccaccacct 1380
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gataccatga gctttcacc tggcggggac tggcaggctt cacaatgtgt gaattcaaa 1620
agttttcct taatggtggc tgcctagagct ttggcccttg cttaggatta ggtggccctc 1680
acaggggtgg ggccatcaca gctccctct gccagctgca tgctgccagt tcctgttctg 1740
tgttcaccac atccccacac cccattgcca cttatttattt catctcagga aataaagaaa 1800
ggtcttggaa agttaaaaaaa aaaaaaaaaa aaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
50 55 60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Asn Leu
65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
355 360 365

Met Phe Phe Gly Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
405 410 415

Ile Lys Gly Arg
420

<210> 110
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 110
cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgta 50

<210> 111
<211> 22
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 112

atctgcttgt agccctcgac ac

22

<210> 113

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1461)..(1461)

<223> a, t, c or g

<400> 113

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cggggccgccc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcaagctaa 180
agaggtgccc accctggaca gggccgacat ggaggagctg gtcatcccc cccacgtgag 240
ggcccagtac gtggccctgc tgcaagcgcag ccacggggac cgctcccgcg gaaagaggtt 300
cagccagagc ttccgagagg tgccggcag gttcctggcg ttggaggcca gcacacacct 360
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gcgcgtcttc caggagccgg tccccaaaggc cgccgtgcac aggacacgggc ggctgtcccc 480
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cgacgtgacc gaggccgtga acttctggca gcagctgagc cggcccccggc agccgctgct 660
gctacaggtg tcgggtcaga gggagcatct gggcccgctg gcgtccggcg cccacaagct 720
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aaagtccctcc accaccactc tggacctaag acctggggtt aagtgtgggt tgtgcatccc 1560
caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114
<211> 366
<212> PRT
<213> Homo sapiens

<400> 114
Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
1 5 10 15
Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
20 25 30
Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
35 40 45
Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
50 55 60
Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
65 70 75 80
Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
85 90 95
His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
100 105 110
Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
115 120 125
Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
130 135 140
Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
145 150 155 160
Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
165 170 175
Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
180 185 190
Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
195 200 205
Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
210 215 220
Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
225 230 235 240
Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Arg Thr
325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 115

aggactgcc a taacttgccct g 21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 116

ataggagttg a a a g c a g c g c t g c 22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg c c g c t a c c g c tactgccagc accgc 45

<210> 118
<211> 1857
<212> DNA
<213> *Homo sapiens*

<400> 118
gtctgttccc aggagtcctt cgccggctgt tggcgtcgt gcctgatcgc gatggggaca 60
aaggcgcaga tcgagaggaa actgttgc ctcttcataat tggcgtatcct gttgtgctcc 120
ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcaaat tcctgagaat 180
aatcctgtga agttgtcctg tgcctactcg ggctttctt ctccccgtgt ggagtggaaag 240
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cagaggctga ggcaggcggc tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
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agctgctcag ggcctggca acaagagca aactccagct caaaaaaaaaaaaaaaa 1857

<210> 119
<211> 299
<212> PRT
<213> *Homo sapiens*

<400> 119
Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
 65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
 85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295

<210> 120
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 120
 tcgcggagct gtgttctgtt tccc

<210> 121
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 121
tgatcgcgat ggggacaaag gcgcaggctc gagaggaaac tgttgtgcct 50

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 122
acacctgggtt caaagatggg 20

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 123
taggaagagt tgctgaaggc acgg 24

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 124
ttgccttact caggtgtac 20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 125
 actcagcagt ggttaggaaag 20

<210> 126
 <211> 1210
 <212> DNA
 <213> Homo sapiens

<400> 126
 cagcgcgtgg ccggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcgcaggatg 60
 gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactag 120
 gcctggaggc cgccgcgagc ccgcgttcca ccccgaccc tcggccaggcc gcaggccca 180
 gctcaggctc gtgcccaccc accaagttcc agtgcgcac cagtgctta tgcgtgcccc 240
 tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
 ggattgagcc atgtacccag aaagggaat gcccacccgc ccctggccctc ccctggccct 360
 gcaccggcgt cagtgactgc tctggggaa ctgacaagaa actgcgcac tgcagccccc 420
 tggcctgcct agcaggcgag ctccgtgca cgctgagcga tgactgcatt ccactcacgt 480
 ggcgcgtgcga cggccaccca gactgtcccg actccagcga cgagctcggc tggaaacca 540
 atgagatcct cccggaaaggg gatgccacaa ccattggggcc ccctgtgacc ctggagatg 600
 tcacctctct caggaatgcc acaaccatgg ggcccccctgt gaccctggag agtgtccct 660
 ctgtcgggaa tgccacatcc tcctctgccc gagaccagtc tggaaaccca actgcctatg 720
 gggttattgc agctgctgcg gtgctcagtg caaggctggc caccggccacc ctccctcctt 780
 tggcctggct ccgagcccgag gaggcgcctcc gcccactggg ttactggtg gccatgaagg 840
 agtccctgct gctgtcagaa cagaagaccc cgctgcctg aggacaagca cttggccacca 900
 ccgtcactca gcccctggcg tagccggaca ggaggagagc agtgcgcgg atgggtaccc 960
 gggcacacca gcccctcagag acctgagttc ttctggccac gtggaaaccc tcggccgg 1020
 tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080
 agcttaggatg gggAACCTGC cacagccaga actgaggggc tggcccccagg cagctccca 1140
 gggtagaaac gcccctgtgc ttaagacact ccctgctgccc ccgtctgagg gtggcgat 1200
 aagttgcctc 1210

<210> 127
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 127
 Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
 1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
 20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
 35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
 50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
 65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95

Lys Gly Gln Cys Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala
225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln
245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 129

ttggttccac agccgagctc gtcg

24

<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc 50

<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1837)..(1837)
<223> a, t, c or g

<400> 131
cccacgcgtc cggctcgct cgctcgca gcggcgca cagaggtcgc gcacagatgc 60
gggttagact ggcgggggaa ggaggcgag gagggaagga agctgcgtc atgagaccca 120
cagactcttg caagctggat gcctctgtg gatgaaagat gtatcatgga atgaacccga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggttcagc tggcgtgtg cttcggccct gcacagctca 300
cggcggggtt cgatgacctt caagtgtgtg ctgaccggg cattcccgag aatggcttca 360
ggaccccccag cggagggggtt ttcttgaag gctctgtac ccgatttac tgccaagacg 420
gattcaagct gaaggcgct acaaagagac tggtttcaa gcattttat ggaaccctag 480
gctggatccc aagtataat tccatctgtg tgcaagaaga ttgcgtatc cctcaaatcg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaatc atcacttg 600
atgaaggatt caagatccgg taccggacc tacacaatat gtttcatca tgtcgcgt 660
atgaaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gccttttca 720
atggctatgt aaacatctct gagctccaga cctcctccc gttggggact gtgatctc 780
atcgctgctt tccggattt aaacttgcgt ggtctgcgt tcttgagtgc ttacaaaacc 840
ttatctggtc gtccagccca cccgggtgcc ttgctctgga agcccaagtc tgcactac 900
ctccaatggt gagtcacgga gattcgtct gccacccgc gccttgcgtcg cgctacaacc 960
acgaaactgt ggtggagtt tactgcgtc ctggctacag cctcaccaggc gactacaagt 1020
acatcacctg ccagtatgga gagtggttc cttcttatca agtctactgc atcaaatcg 1080
agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaaagatt gtggcggtca 1140
cgccaaccag tggctgcgtg gtgctgcgtc tcgtcatcct gcccaggatg ttccagacca 1200
agtcaaggc ccactttccc cccagggggc ctccggag ttccagcagt gaccctgact 1260
ttgtgggtgt agacggcggtc cccgtcatgc tcccgctcta tgacgaagct gtgagtggcg 1320
gcttgagtgc cttagcccc ggtacatgg cctctgtggg ccaggcgctgc cccttacccg 1380
tggacgacca gagcccccca gcataccccc gctcaggggc cacggacaca ggcccagggg 1440
agtcaaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
ctcccagggtc ccaagagagc acccaccctg cttcgacaa ccctgacata attgccagca 1560
cgccagagga ggtggcatcc accagcccg gcatccatca tgcccactgg gtgttgc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctt tcaaatacat 1680
gttgatctgt ggagttgatt ccttccttc tcttgggttt agacaaatgt aaacaaagct 1740
ctgatccta aaattgctat gctgatagag tggtgaggc tggaaagctt atcaagtcc 1800
gttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490
<212> PRT
<213> Homo sapiens

<400> 132
Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
1 5 10 15
Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
20 25 30
Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
35 40 45
Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
50 55 60
Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
65 70 75 80
Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
85 90 95
Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
100 105 110
Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
115 120 125
Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
130 135 140
Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
145 150 155 160
Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
165 170 175
Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn
180 185 190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr
195 200 205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys
210 215 220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu
225 230 235 240
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe
245 250 255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val
260 265 270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr

275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
320		
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
400		
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
450		
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
455	460	
Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His		
465	470	475
480		
His Ala His Trp Val Leu Phe Leu Arg Asn		
485	490	
<210> 133		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 133		
atccctatc gctgcttcc cg		
23		
<210> 134		
<211> 23		
<212> DNA		
<213> Artificial Sequence		

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134
 agccaggatc gcagtaaaac tcc

23

<210> 135
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135
 atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct

50

<210> 136
 <211> 1815
 <212> DNA
 <213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctccgtg cggtccgtcg gtggcctaga 60
 gatgctgctg ccgcgggttgc agttgtcgcg cacgcctctg cccgcccagcc cgctccaccg 120
 ccgttagcgcc cgagtgtcgg ggggcgcacc cgagtcggc catgaggccg ggaaccgcgc 180
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtgcgcctgc 240
 tgagtgccctc ggatttggac ctcagaggag ggcagccagt ctgcccggga gggacacaga 300
 ggcttgtta taaagtcttacttccatg atacttctcg aagactgaac tttgaggaag 360
 ccaaagaagc ctgcaggagg gatggaggcc agcttagtcg catcgagtct gaagatgaac 420
 agaaaactgtat agaaaagttc attgaaaacc tcttgcacatc tgatgggtgac ttctggattg 480
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgcccaggac ctttatgctt 540
 ggactgatgg cagcatatca caattttaga actggtatgt ggatgagccg tcctgcggca 600
 gcgaggctcg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggaggccct 660
 acatgttcca gtggaatgtat gaccgggtgca acatgaagaa caatttcatt tgcaaataatt 720
 ctgatgagaa accagcagtt cttcttagag aagctgaagg tgagggaaaca gagctgacaa 780
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaaagta 840
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattcccccctt ctccctcctcc 900
 ttgtggtcac cacagtgttga tgggggttt ggatctgtag aaaaagaaaa cgggagcagc 960
 cagacccttag cacaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
 ggccagacct gaagaatatt tcattccgag tgggttcggg agaagccact cccgatgaca 1140
 tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggtt gtgactctgg 1200
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaatgg 1260
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
 aaactgtaaac tgacaacaat ggaaaagaaa tgataagcaa aatccctctt ttttctataa 1380
 ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
 tccccacgac ctccctgttgg acccccacgt tttggctgttgc tcctttatcc cagccagtca 1500
 tccagctcgat ccttatgaga agtacatgg cccaggtctg gcacatagta gagtctcaat 1560
 aaatgtcaact tgggtgggtt tatctaactt ttaagggaca gagtttacc tggcagtgtat 1620
 aaagatgggc tggagcattt gggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
 atattatcat acagacagaa aatccagaat ctttcaaaag cccacatatg gtagcacagg 1740
 ttggcctgtg catcggaat tctcatatct gttttttca aagaataaaa tcaaataaaag 1800
 agcagggaaaa aaaaaa

1815

<210> 137
<211> 382
<212> PRT
<213> Homo sapiens

<400> 137
Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
1 5 10 15
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
20 25 30
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
35 40 45
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
50 55 60
Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
65 70 75 80
Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
85 90 95
Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
100 105 110
Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
115 120 125
Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
130 135 140
Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
145 150 155 160
Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
165 170 175
Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
180 185 190
Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
195 200 205
Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
210 215 220
Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
225 230 235 240
Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
245 250 255
Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
260 265 270

Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
275 280 285

Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
290 295 300

Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
305 310 315 320

Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
325 330 335

Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
340 345 350

Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
355 360 365

Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
370 375 380

<210> 138

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 138

gttcattgaa aacctttgc catctgatgg tgacttctgg attgggctca 50

<210> 139

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 139

aagccaaaga agcctgcagg aggg 24

<210> 140

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 140

cagtccaaagc ataaagggtcc tggc 24

<210> 141
<211> 1514
<212> DNA
<213> Homo sapiens

<400> 141
gggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
gcatccgcag gttccgcgg acttggggc gcccgttag ccccgccgccc cgagaagac 120
ttgtgttgc ctccctgcagc ctcacccgg agggcagcga gggcttacca ccatgatcac 180
tgggtgttgc agcatgcgct tggggccccc agtgggcgtc ctgacccgc tggctactg 240
cctgcaccag cggcggtgg ccctggccga gctgcaggag gccgatggcc agtgcgggt 300
cgaccgcagc ctgctgaagt taaaatggt gcaggtcgtt ttcgacacg gggctcgag 360
tcctctcaag ccgctccgc tggaggagca ggtagagtgg aaccccccagc tattagaggt 420
cccaccccaa actcaggttt attacacagt caccaatcta gctgggtgtc cgaaaccata 480
tttccttac gactctaat accatgagac caccctgaag gggggcatgt ttgctggca 540
gctgaccaag gtgggcattgc agcaaatgtt tgccttgggagagactga ggaagaacta 600
tgtgaaagac attcccttc ttcaccaac cttcaacccca caggaggatct ttattcggtc 660
cactaacatt ttccgaaatc tggagtccac ccgttgggttgc tggctgggc tttccagtg 720
tcagaaagaa ggacccatca tcatccacac tcatgaagca gattcagaag tcttgatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttggaa aaaggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcaccccttgc ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgccccatgc tgaagagatt tgcacggatgc atcgaacaga gagctgtgga 1020
cacatccttgc tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggccc 1080
attccctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccca 1140
caagatcaga aagctgtatc tctatgcggc tcatgtatgt accttcatac cgctcttaat 1200
gaccctgggg attttgcacc acaaatggcc accgttgcgtt gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggtt tgcacccatgc tattaccacg ggaaggagca 1320
ggtgcgaga gttgcctg atggctctg cccgctggac atgttcttgc atgcctatgtc 1380
agtttataacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agtggaaat gaagagtaac tgatttataa aagcaggatg tggtgattt aaaataaaagt 1500
gccttatac aatg 1514

<210> 142
<211> 428
<212> PRT
<213> Homo sapiens

<400> 142
Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
165 170 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile His
180 185 190

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
195 200 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
210 215 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
225 230 235 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
245 250 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
260 265 270

Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
275 280 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
290 295 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
305 310 315 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
325 330 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
340 345 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
355 360 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
370 375 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
385 390 395 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
405 410 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
420 425

<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143
ccaactacca aagctgctgg agcc 24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144
gcagctctat taccacggga agga 24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145
tccttcccggt ggtaatagag ctgc 24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146
ggcagagaac cagaggccgg aggagactgc ctcttacag ccagg 45

<210> 147
<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctccctttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttcttagc 60
cttaaatttc agtcatcac cttcacctgc cttggatcatg gctctgtat tctccttgat 120
ccttgcatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtgg 180
gggcctccac cgctgtgaag ggcgggtgga ggtggAACAG aaaggccagt gggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgtt tgccgggagc tggctgtgg 300
agctgccagc ggaacccta gtggatttt gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcatc caatcagtca gtgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgtgg gcacgtgtg agaaccaga 480
gagcttttc tccccagttcc cagaggggtt caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccgggcc gcaaagggtgg tggccggca gctggatgt gggagggctg tactgactca 660
aaaacgcgtc aacaagcatg cctatggccg aaaaccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaaggattt cccttctggg cttgggggaa agaacacactg 780
caaccatgat gaagacacgt ggtcgaatg tgaagatccc tttgacttga gacttaggg 840
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cattctaca cacacacaca cacacacaca cacacataca ccatttgc 1500
tgtttctctg aagaactctg acaaaaataca gatttggta ctgaaagaga ttctagagga 1560
acgaaatttt aaggataaat tttctgaatt gtttatgggg tttctgaaat tggctctata 1620
atctaatttag atataaaattt ctggtaactt tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Asp Asn Leu Cys Ser Gly Arg
245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 149	
ttcagctcat cacccatcacc tgcc	24
<210> 150	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 150	
ggctcatac aataaccact aggg	24
<210> 151	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 151	
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt	50
<210> 152	
<211> 1427	
<212> DNA	
<213> Homo sapiens	
<400> 152	
actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgaccccg 60	
accacacgcgt ccgcggacgc gtggcgacgc gcgtggccg gctaccagga agagtctgcc 120	
gaaggtgaag gccatggact tcataccatc cacagccatc ctgccttcgc tgccggctg 180	
cctggcgctc ttccgcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240	
gaatgctgtg gtggatca caggcgccac ctcagggctg ggcaaaagaat gtcaaaagt 300	
cttctatgct gcgggtgcta aactgggtct ctgtggccgg aatgggtgggg ccctagaaga 360	
gctcatcaga gaacttaccg cttctatgc caccaaggtg cagacacaca agccttactt 420	
ggtagccctc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480	
gtgtttggc tatgtcgaca tactgtcaa caatgctggg atcagctacc gtggtaccat 540	
catggacacc acagtggatg tgacaagag ggtcatggag acaaactact ttggcccgat 600	
tgctctaact aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660	
catcagcagc atccagggca agatgagcat tcctttcga tcagcatatg cagcctccaa 720	
gcacgcaacc caggcttct ttgactgtct gcgtggcgag atggAACAGT atgaaattga 780	
ggtagccgtc atcagccccg gctacatcca caccaacctc tctgtaaatg ccatcaccgc 840	
ggatggatct aggtatggag ttatggacac caccacagcc caggccgaa gcccgtgga 900	
ggtagcccgat gatgttcttgc ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960	
cttactgcct tccttggtct tttatcttcg aactctggct cctggctct tcctcagcc 1020	
catggcctcc agggccagaa aagagcgaa atccaagaac tccttagtact ctgaccagcc 1080	
agggccaggc cagagaagca gcactcttag gcttgcctac tctacaagg acagttgcat 1140	
ttgttgagac ttatggag atttgtctca caagtggaa agactgaaga aacacatctc 1200	
gtgcagatct gctggcagag gacaatcaa aacgacaaca agcttcttcc cagggtgagg 1260	
ggaaacactt aaggaataaa tatggagctg gggtaaca ctaaaaacta gaaataaaca 1320	
tctcaaacag taaaaaaaaaaa aaaaaaggc ggccgcgact ctagagtcga cctgcagaag 1380	

cttggccgcc atggcccaac ttgttattg cagttataa tggttac 1427

<210> 153
<211> 310
<212> PRT
<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr
210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
225 230 235 240

Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val

260

265

270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu
290 295 300

Arg Lys Ser Lys Asn Ser
305 310

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154
ggtgctaaac tggtgctctg tgcc 24

<210> 155
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155
cagggcaaga tgagcattcc 20

<210> 156
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 156
tcatactgtt ccatctcgcc acgc 24

<210> 157
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 157

aatgggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158

<211> 1771

<212> DNA

<213> Homo sapiens

<400> 158

cccacgcgtc cgctgggtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaaa acacaccaaa cgctcgacg cacaaggatggc atgaaatttc ttctggacat 120
cctcctgctt ctcccgttac tgatcgctg ctcccttagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcgctgatt accaggag ctgggcatgg 240
aattgggaga ctgactgcct atgaatttgc taaaacttaaa agcaagctgg ttctctgggaa 300
tataaataag catggactgg aggaaacacgc tgccaaatgc aagggactgg gtgccaagg 360
tcataccttt gtggtagact gcagcaaccc agaagatatt tacagctctg caaagaagg 420
gaaggcagaa attggagatg ttagtattt agtaataat gctgggttag tctatacatc 480
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagttt atgtacttgc 540
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
tgtcactgtg gcttcggcag ctggacatgt ctcggcccc ttcttactgg cttactgttc 660
aagcaagtt gctgctgtt gatttcataa aactttgaca gatgaactgg ctgccttaca 720
aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780
aaatccaagt acaagttgg gaccactct ggaacctgag gaagtggtaa acaggctgat 840
gcatgggatt ctgactgagc agaagatgtat ttttattcca tcttctatag ctttttaac 900
aacattggaa aggatccctc ctgagcgtt cctggcagtt taaaacgaa aaatcagtgt 960
taagttttagt gcagttattt gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020
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cttctgtttt ttcttaattt cccatttct tcaatatcat ttttgaggct ttggcagtct 1140
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tacctttaga ggtgacttta agaaaaatga agaaaaaagaa cccaaatgac tttttaaaa 1260
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gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggatttgc aggagaattt 1620
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaaa 1680
aaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1771

<210> 159

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Pro Leu Leu Ile Val
1 5 10 15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
 65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
 85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
 100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
 115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
 130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
 145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
 165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
 180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
 195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
 210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
 225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
 245 250 255

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 160
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 160
 ggtgaaggca gaaattggag atg

<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 161
atcccatgca tcagcctgtt tacc 24

<210> 162
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 162
gctggtag tctatacatc agattgttt gctacacaag atcctcag 48

<210> 163
<211> 2076
<212> DNA
<213> Homo sapiens

<400> 163
cccacgcgtc cgcggacgacg tgggtcgact agttctagat cgcgagcggc cgccgcggc 60
tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaaggtg 120
attgtttcgc tggctctgtt gatgcctggc ccctgtatgg ggctgtttcg ctccctatac 180
agaagtgttt ccatgccacc taaggagac tcaggacagc cattattct cacccttac 240
atgaagatgt ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttccagga 300
ctgaacatga agagttatgc cgcttcctc accgtataa agacttacaa cagcaacctc 360
ttcttctggc tcttcccagc tcagatacag ccagaagatg cccctggatgt tctctggcta 420
caggggtggc cgggaggttc atccatgttt ggactctttg tggaaacatgg gccttatgtt 480
gtcacaagta acatgacccctt gggtgacaga gacttccctt ggaccacaac gctctccatg 540
ctttacattt acaatccatg gggcacaggc ttcagttta ctgatgatac ccacggatat 600
gcagtcaatg aggacgatgt agcacggat ttatacagtg cactaattca gttttccag 660
atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctt tgcagggaaa 720
tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
aacctgaacg gaattgttat tgagatgga tattctgatc cccaatcaat tatagggggc 840
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aaaggatggg atccttatgt tgataaaact accttccaa aagagaacat cagaggtttt 1560
cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaaa aattatcttt 1620

tcatatctgc aagattttt tcatcaataa aaattatcct taaaacaagt gagctttgt 1680
ttttgggggg agatgttac taaaaat aacatgagtaat atgagtaaga attacattat 1740
ttaactaaa ggatgaaagg tatggatgt gtgacactga gacaagatgt ataaatgaaa 1800
ttttagggtc ttgaatagga agtttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860
taacaaacaa agctgtaca tcttttctg ccaataacag aagtttggca tgccgtgaag 1920
gtgttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaaattt gtataaagtc tttagaacaaa agaattcttt 2040
gaaataaaaaa tattatataat aaaagtaaaaa aaaaaa 2076

<210> 164
<211> 476
<212> PRT
<213> Homo sapiens

<400> 164
Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val
65 70 75 80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln
85 90 95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro
100 105 110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
115 120 125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
130 135 140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
145 150 155 160

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
165 170 175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
180 185 190

Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
195 200 205

Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
210 215 220

Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
225 230 235 240

Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
245 250 255

Gly Leu Leu Asp Glu Lys Gln Lys Tyr Phe Gln Lys Gln Cys His
260 265 270

Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu
275 280 285

Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
290 295 300

Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
305 310 315 320

Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
325 330 335

Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
340 345 350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
465 470 475

<210> 165
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 165
ttccatgcc a cctaaggag actc 24

<210> 166
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 166
tggatgagg t gtgcaatggc tggc 24

<210> 167
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167
agctctcaga ggctggtcat aggg 24

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gtttcctcac 50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
cgagggctt tccggctccg gaatggcaca tgtggaaatc ccagtcttgt tggctacaac 60
attttccct ttcctaacaa gttctaacag ctgttctaac agctagtat caggggttct 120
tcttgcttga gaagaaaggg ctgagggcag agcagggcac tctactcag ggtgaccagc 180
tccttgcctc tctgtggata acagagcatg agaaagtgaa gagatgcagc ggagttaggt 240
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<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

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 20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
 35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
 50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
 65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
 85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
 100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
420 425 430
Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
435 440 445
Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn
450 455 460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
465 470 475 480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
485 490 495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
500 505 510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
515 520 525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
530 535 540
Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171
tggaaataccg cctcctgcag 20

<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172
cttctgccct ttggagaaga tggc 24

<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173
ggactcactg gcccaggcct tcaatatcac cagccaggac gat 43

<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens

<220>
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<222> (1683)..(1683)
<223> a, t, c or g

<400> 174
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tgctggctgt ctggggcttc ctgggtctcc gcaggctgga ctggagcacc ctgggtccctc 180
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tgaggctgAG gacaacttAC aagggcttCA ccgaAGCAGT ggacctttat tttgaccacc 600
tgatgtccAG ggtgggtGCCA ctccAGTACA AGCgtggggG acctatcatt gccgtgcagg 660
tggagaatGA atatggttCC tataataaAG accccgcATA catgccctAC gtcaagaagg 720
caCTggagGA ccgtggcATT gtggAACTGC tcctgacttC agacaacaAG gatgggctGA 780
gcaaggggat tgcggcggA gtcggcggCA ccatcaactt gcagtcaaca cacgagctgc 840
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
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Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
145 150 155 160

Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp

165

170

175

His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
180 185 190

Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
195 200 205

Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
210 215 220

Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
225 230 235 240

Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
245 250 255

Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
260 265 270

Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
275 280 285

Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
290 295 300

Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
305 310 315 320

Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
325 330 335

Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
340 345 350

Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
355 360 365

Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
370 375 380

Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
385 390 395 400

Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
405 410 415

Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val

465	470	475	480
Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn			
485	490	495	
Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp			
500	505	510	
Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser			
515	520	525	
Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr			
530	535	540	
Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr			
545	550	555	560
Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val			
565	570	575	
Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln			
580	585	590	
Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln			
595	600	605	
Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr			
610	615	620	
Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys			
625	630	635	
<210> 176			
<211> 2505			
<212> DNA			
<213> Homo sapiens			
<400> 176			
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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

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20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro
225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile
340 345 350

Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro
355 360 365

Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu
370 375 380

Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu
385 390 395 400

Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr
405 410 415

Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val
420 425 430

Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val
435 440 445

Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr
450 455 460

Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg
465 470 475 480

Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro
485 490 495

Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu
500 505 510

Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys
515 520 525

Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr
530 535 540

Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly
545 550 555 560

Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr
565 570 575

Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu
580 585 590

Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu
595 600 605

Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu
610 615 620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
645 650

<210> 178
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 178
tggctactcc aagaccctgg catg 24

<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 179
tggacaaatc cccttgctca gccc 24

<210> 180
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 180
gggcttcacc gaagcagtgg acctttatgg tgaccacctg atgtccaggg 50

<210> 181
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 181
ccagctatga ctatgatgca cc 22

<210> 182
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182
tggcacccag aatggtgttg gctc 24

<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183
cgagatgtca tcagcaagtt ccaggaagtt ccttgggac ctttacctcc 50

<210> 184
<211> 1947
<212> DNA

<213> Homo sapiens

<400> 184

gcttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60
gcacccacaa tatggcttac atgtgaaaa agcttctcat cagttacata tccattattt 120
gtgttatgg ctttatctgc ctctacactc tcttctggtt attcaggata cctttgaagg 180
aatattctt cggaaaaagtc agagaagaga gcagtttag tgacattcca gatgtcaaaa 240
acgatttgc gttccttctt cacatggtag accagtatga ccagctata tccaagcggt 300
ttggtgtgtt cttgtcagaa gtttagtggaa ataaacttag ggaaatttagt ttgaaccatg 360
agtggacatt tgaaaaactc aggacgaca tttcacgcaa cgcccaggac aagcaggagt 420
tgcacatgtt catgctgtcg ggggtgcccgc atgctgtctt tgacactaca gacctggatg 480
tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
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ttcttcgcga tcacttgaga tgcccttcacg tgaagttcac tgatgtggct gaaattcctg 660
cctgggtgta tttgctaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
aaaacaataa gatgatagga ctgaaatctc tccgagagtt gcggcacctt aagattctcc 780
acgtgaagag caatttgacc aaagtccct ccaacattac agatgtggct ccacatctta 840
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agggaaaggaa aaattataat cactaatctt ggttctttt aaattgtttg taacttggat 1860
gctgccgcta ctgaatgttt acaaatttgc tgcctgctaa agtaaatgat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaaaaa 1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
1 5 10 15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
20 25 30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
35 40 45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
50 55 60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
65 70 75 80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
85 90 95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
100 105 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
115 120 125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
130 135 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
145 150 155 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
180 185 190

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr
465 470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro
485 490 495

Phe Ala Asn Gly Ile
500

<210> 186
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 186
cctccctcta ttacccatgt c 21

<210> 187
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 187
gaccaacttt ctctgggagt gagg 24

<210> 188
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 188

gtcactttat ttctctaaca acaagctcga atccttacca gtggcag

47

<210> 189

<211> 2917

<212> DNA

<213> Homo sapiens

<400> 189

cccacgcgtc cggccttctc tctggacttt gcatttccat tcctttcat tgacaaaactg 60
actttttta tttctttttt tccatctctg ggccagcttggatcctagg ccgccttggg 120
aagacatttg tgttttacac acataaggat ctgtgtttgg gtttcttct tcctccctg 180
acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
gcacttatct gccttaggtac atcgaagtct tttgacctcc atacagtat tatgcctgtc 300
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cacaacccag acaaggtgtg gtgggccaag aacagccagg cccaaaaccat tgccacggag 480
tcttgcctg ccctgcagtg ctgtgaagga tatagaatgt gtgcctgtt tgattccctg 540
ccacccgtc gttgcgacat aaatgaggcct ctctgagttt gggaaaggctc cttctcaaa 600
gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgcgtat gtgcaggcac 660
agaagaaagg cacagctccc catcagttt atggaaaata actcagtgcc tgctggaaac 720
cagctgctgg agatccctac agagagctt cactggggc aacccttcca ggaaggagtt 780
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aacttgcac taaaagaccc aacttgcaga cccaaattt caaatgtgtt ggaattttct 1920
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cagattattt tgaagtgtgtt aatgggacat aattctacag tggagataat atacataaaca 2100
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aaataccaga agctgcagaa ctatataacta acaggtccaa cccttaatgtt gacatgtttc 2820

tccaggatgc caaaggaaat gctacctcggt ggctacacat attatgaata aatgaggaag 2880
ggcctgaaag tgacacacag gcctgcatgt aaaaaaaaaa 2917

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
130 135 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
145 150 155 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
165 170 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
180 185 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
195 200 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
210 215 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
225 230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
500 505 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
530 535 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val
565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr
595 600 605

<210> 191
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 191
tctctattcc aaactgtggc g 21

<210> 192
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 192
tttgatgacg attcgaaggt gg 22

<210> 193
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 193
ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194
<211> 2362
<212> DNA
<213> Homo sapiens

<400> 194
gacggaagaa cagcgctccc gagggccgcgg gagcctgcag agaggacagc cggcctgcgc 60
cgggacatgc ggccccagga gctccccagg ctcgcgttcc cggtgctgct gttgctgttg 120
ctgctgctgc cgccgcccgttcc cacagcgcca cgcgcgttcc ccccacctgg 180
gagtccctgg acgccccgcca gctgccccggc tggtttgacc aggccaaatggc cggcatcttc 240
atccactgggg gagtgttttc cgtgccccggc ttccggtagcg agtgggttctg gtggatttgg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360

aaatatgaag attttggacc actattaca gcaaaattt ttaatgccaa ccagtggca 420
gatattttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
tttaccttgc ggggtcaga atattcgtgg aactgaaatg ccatagatga ggggcccag 540
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aacagcacag gcttcttggc ctggttataat aatgaaagcc cagttcgggg cacagtagtc 840
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gaatttgggg tattatggac cgaactgaaa atttatgtt gaagccatata ccccatgat 1800
tatatagtt tgcacactt aatatgggg tattttctgg gaaatgcatt gctagtcaat 1860
ttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920
cacacctaattt gtgtatggta tagactgtt ctcctaggct acagacatata acagcatgtt 1980
actgaataact gtaggcaata gtaacagtgg tattttgtata tcgaaacata tggaaacata 2040
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taggacatta ttgaacactg ccagacgtt taaataactgt atgcttaggc tacactacat 2220
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taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu
1 5 10 15

Leu Leu Leu Leu Pro Pro Pro Cys Pro Ala His Ser Ala Thr
20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro

85

90

95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu

385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
450 455 460

Asn Val Ile
465

<210> 196
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 196
tggtttgacc aggccaagtt cg 23

<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 197
ggattcatcc tcaaggaaga gc 24

<210> 198
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 198
aacttgcagc atcagccact ctgc 24

<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 199

ttccgtgccc agcttcggta gcgagtggtt ctgggtggat tggca

45

<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

agcaggaaa tccggatgtc tcggttatga agtggagcag tgagtgttag cctcaacata 60
gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120
catctgaggt gtttccctgg ctctgaaggg gttaggcacga tggccaggtg cttcagcctg 180
gtttgtctc tcacttccat ctggaccacg aggctcctgg tccaaggctc tttgcgtgca 240
gaagagctt ccatccaggt gtcatgcaga attatggga tcacccttgc gagcaaaaag 300
gcgaaccagc agctgaattt cacagaagct aaggaggcct gttaggctgct gggactaagt 360
ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
ggctgggtt gagatggatt ctgtgtcatc tctaggatta gcccaaacc ccaagtgtggg 480
aaaaatgggg tgggtgtcct gatttggaaag gttccagtga gccgacagtt tgccgcctat 540
tgttacaact catctgatac ttggactaac tcgtgcattc cagaattt caccacaaa 600
gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcacat 660
acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720
ccagcttcca cttcttattcc acggagaaaa aaattgattt gtgtcacaga agttttatg 780
gaaactagca ccatgtctac agaaaactgaa ccatttggtaaaa aataaaagc agcattcaag 840
aatgaagctg ctgggtttgg aggtgtcccc acggctctgc tagtgcttgc tctccttcc 900
tttgggtctg cagctggctt tggattttgc tatgtcaaaa ggtatgtgaa ggccttccct 960
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gccaatgata gcaaccctaa tgaggaatca aagaaaaactg ataaaaacc cagaagagtcc 1080
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caaggagtca ctgagaccaa ggcttcttctt actgattccg cagctcagac ctttcttca 1560
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agggaaatata ctttacaag taacaaaaat aaaaacttctt ataaatttctt atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcagg tattacactc 2040
tgtaattgaa tattttctt caaaaaattt cacatgttag aacgctatctt gggagctat 2100
ttttttcagt ttgtatattt cttagcttac tacttccaaa ctaatttttta tttttgctga 2160
gactaatctt attcattttc tctaataatgg caaccattat aaccttaattt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaaagca cattttaaaa gtgcattaa 2280
caaatgtatc actagccctc cttttccaa caagaaggaa ctgagagatg cagaaatattt 2340
tgtgacaaaaa aattaaagca tttagaaaaac tt 2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
1 5 10 15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
165 170 175

Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
195 200 205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
210 215 220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
225 230 235 240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
245 250 255

Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
260 265 270

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
275 280 285

Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
290 295 300

Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
305 310 315 320

Glu Val

<210> 202
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202
gagctttcca tccaggtgtc atgc 24

<210> 203
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 203
gtcagtgaca gtacctactc gg 22

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 204
tggaggcagga ggagtagtag tagg 24

<210> 205
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 205
 aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50

 <210> 206
 <211> 1620
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (973)..(973)
 <223> a, t, c or g

 <220>
 <221> modified_base
 <222> (977)..(977)
 <223> a, t, c or g

 <220>
 <221> modified_base
 <222> (996)..(996)
 <223> a, t, c or g

 <220>
 <221> modified_base
 <222> (1003)..(1003)
 <223> a, t, c or g

 <400> 206
 agatggcgggt cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
 ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
 ggaaactgccc gcccgtctgc cacggctctgc ccacccaacg cgaagacgggt aaccctgtg 180
 actttgactg gagagaagtg gagatcctga tgtttctcgt tgccattgtg atgatgaaga 240
 accgcagatc catcaactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
 ccaacacaat tctttcttc cgcttggata ttgcgtatggg cctactttac atcacactct 360
 gcatagtgtt cctgtatgacg tgcaaaacccc ccctatataat gggcccttag tatataaagt 420
 acttcaatga taaaaccatt gatgaggaac tagaacggga caagagggtc acttggattg 480
 tggagttctt tgccaattgg tctaattgact gccaatcatt tgcccctatc tatgtgtacc 540
 tctcccttaa atacaactgt acagggtctaa attttggaa ggtggatgtt ggacgctata 600
 ctgtatgttag tacgcggtagc aaagttagca catcaccctt caccaagcaa ctccctaccc 660
 tgatcctgtt ccaagggtggc aaggaggcaa tgccggggcc acagattgac aagaaaggac 720
 gggctgtctc atggacacctc tctgaggaga atgtgatccg agaatttaac ttaaatgagc 780
 tataccagcg ggccaagaaaa ctatcaaagg ctggagacaa tatcccttag gagcagcctg 840
 tggcttcaac cccccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
 actttggcag tgcttcctct cctgtcaatt ccaggcttcc tccataacca caagccttag 960
 gctgcagct ttnattnatg tttccctt ggctngact ggntggggca gcatgcagct 1020
 tctgattttta aagaggcatc tagggaattt tcaggcaccc tacaggaagg cctgcccattgc 1080
 tggcccaac tgtttactg gagcaagaaa gagatctcat aggacggagg gggaaatgg 1140
 ttccctccaa gcttgggtca gtgtgttaac tgctttagtgc ctattcagac atctccatgg 1200
 tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagctgggtt 1260
 agaccttagat ttaaccctaa ggtaagatgc tggggatag aacgctaaga attttcccc 1320
 aaggactctt gcttccttaa gcccttctgg cttcgatgtt ggtcttcatc aaaagtataa 1380
 gcctaacttt gtcgttagtc ctaaggagaa acctttaacc acaaagttt tatcattgaa 1440
 gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
 acttccttt gtgtggtagg acttggagga gaaatcccct ggacttccac taaccctctg 1560
 acatactccc cacacccttgc tgcataaaaa aagattggga tttccctttt 1620

<210> 207
<211> 296
<212> PRT
<213> Homo sapiens

<400> 207
Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
1 5 10 15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys
290 295

<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 208
gcttggatat tcgcataatggc ctac 24

<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 209
tggagacaat atccctgagg 20

<210> 210
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 210
aacagttggc cacagcatgg cagg 24

<210> 211
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 211
ccattgtga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
<211> 1985

<212> DNA
<213> Homo sapiens

<400> 212
ggcacgctcg cgccccccga gagctctagc cgtcgaggag ctgcctgggg acgttgc 60
tggggcccca gcctggcccg ggtcacccctg gcatgaggag atggccctgt tgctcctggt 120
cccattgctc ctgctggcccg gtcctacgg actgccttc tacaacggct tctactactc 180
caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240
gaagctggtg gtggagacac ccgaggagac cctgttacc taccaagggg ccagtgtat 300
cctgcctgc cgctaccgct acgagccggc cctggtctcc cgcggcg 360
atggtggaaag ctgtcgaga acggggccccc agagaaggac gtgctgggtgg ccatcg 420
gaggcaccgc tcctttgggg actaccaagg cccgctgcac ctgcggcagg acaaagagca 480
tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540
ggtcattgac gggctggagg atgaaagcgg tctggtggag ctggagctgc ggggtgtggt 600
cttccttac cagtc 660
ctgtgc 720
gggcctggac tggtaac 780
gttgc 840
ccgcccaccgc cgctgcacc gctatgatgt attctgc 900
ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaagg 960
ggaagatgat gccacgatcg ccaagg 1020
cctggaccgc tgcacgctg gctggctggc agatggc 1080
cccgcatcct aactgtggc ccccagagcc tgggtccga agctt 1140
gcagagccgc ttgtacggtg ttactgcta ccc 1200
tgccgcattc cctca 1260
agccattta actgtttta tacttctcaa tt 1320
tttttgtaa agcaaacaga acccaatg 1380
aatcatgctt gctcccctgg gccattg 1440
atccaggctg gtctccctc ctt 1500
agaatgccgc cggagtcg ggcattgtgg 1560
gaagaagagg gcctcg 1620
cttctctgtg aagccgctga ccc 1680
tctaggcttc caggc 1740
ctctcggttc caaagaatct gttt 1800
aggggcctc aggtgtgt 1860
aaaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1920
aaaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1980
aaaaaa 1985

<210> 213
<211> 360
<212> PRT
<213> *Homo sapiens*

<400> 213
Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp
115 120 125

Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr
130 135 140

Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Ser Gly Leu Val Glu
145 150 155 160

Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg
165 170 175

Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala
180 185 190

Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly
195 200 205

Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr
210 215 220

Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro
225 230 235 240

Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp
245 250 255

Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu
260 265 270

His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu
275 280 285

Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys
290 295 300

Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser
305 310 315 320

Val Arg Tyr Pro Val Val His Pro Asn Cys Gly Pro Pro Glu
325 330 335

Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr
340 345 350

Gly Val Tyr Cys Tyr Arg Gln His
355 360

<210> 214
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214
tgcttcgcta ctgccctc 18

<210> 215
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 215
ttcccttgtg ggttggag 18

<210> 216
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 216
aggctggaa gccagttc 18

<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 217
agccagttag gaaatgcg 18

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 218
tgtccaaagt acacacacacct gagg

24

<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 219
gatgccacga tcgccaagggt gggacagctc tttgccgcct ggaag

45

<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 220
ggagagcggg gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60
gcttctgttg ctactgaggc acggggccca ggggaagcca tccccagacg caggccctca 120
tggccagggg aggggtcacc accggggccc cctgagcgcac gctcccccatt atgacgccc 180
cgggaacttc cagtagcacc atgaggctt cctgggacgg gaagtggcca aggaattcga 240
ccaactcacc ccagaggaaa gccaggcccg tctgggacgg atcgtggacc gcatggaccg 300
cgcgggggac ggcgacggct ggggtcgct ggccgagctt cgccgctggta tcgcgcacac 360
gcagcagcgg cacatacggg actcggtgag cgccggctgg gacacgtacg acacggaccg 420
cgacgggcgt gtgggttggg aggagctcgca caacgccacc tatggccact acgcgcccgg 480
tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540
gcggcgttcc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600
agccttcctg caccggcagg agttccctca catgcgggac atcgtgattt ctgaaaccct 660
ggaggacctg gacagaaaaca aagatggcta tgtccagggt gaggagtaca tcgcggatct 720
gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780
ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tggccactg 840
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cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggttaatt ggaacatgtt 960
tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020
agcaccgcgc acctgccacca gcctcagagg cccgcacaaat gacccggagga gggccgctg 1080
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ccagggaggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtcctc 1260
cagccccagac ccagggaccc ttggcccaa gctcagctt aagaaccgccc ccaacccttc 1320
cagctccaaa tctgagcctc caccacatag actgaaactc ccctggcccc agccctctcc 1380
tgccctggcct ggcctggac acctcctctc tgccaggagg caataaaagc cagcggccggg 1440
accttggaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaa 1503

<210> 221
<211> 328
<212> PRT
<213> Homo sapiens

<400> 221
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His
1 5 10 15

Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly
20 25 30

Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala
35 40 45

His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val
50 55 60

Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu
65 70 75 80

Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
85 90 95

Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg
100 105 110

His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp
115 120 125

Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly
130 135 140

His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
145 150 155 160

Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp
165 170 175

Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
180 185 190

His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
195 200 205

Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
210 215 220

Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Pro Ala
225 230 235 240

Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
245 250 255

Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
260 265 270

Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
275 280 285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
305 310 315 320

Leu Thr Arg His His Asp Glu Leu
325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 225

ccccccctgag cgacgctccc ccatgatgac gccccacggga actt

44

<210> 226

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 226

gggccttc cttccgact cggcgcagc cgggtggatc tcgagcaggc gcggagcccc 60
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 ccagcctgtc tgcgtcggtt ttggccccc cgccctcccc cggtgcgggg ttgcacaccg 180
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<210> 227
 <211> 550
 <212> PRT
 <213> Homo sapiens

<400> 227
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Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
 20 25 30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
 35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
145 150 155 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
245 250 255

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
530 535 540

Phe Leu Glu Ser Gln Gln
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228

tggctcgca caccgatc 18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 229
ctgctgtcca caggggag 18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 230
ccttgaagca tactgctc 18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 231
gagatagcaa tttccgcc 18

<210> 232
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 232
ttcctcaaga gggcagcc 18

<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 233
cttggcacca atgtccgaga tttc 24

<210> 234
<211> 45
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 234

gctctgagga aggtgacgct cggggcctcc gaacccttgg ctttg

45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235

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gtcgccggcg cggctcgccg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180
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aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580
aaaaaaaaa 2586

<210> 236
<211> 350
<212> PRT
<213> Homo sapiens

<400> 236

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Ala Ala Ala
1 5 10 15

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
325 330 335

Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
340 345 350

<210> 237

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

ggagctgcac cccttgc

17

<210> 238

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 238

ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg

49

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 239

gcagagcgg aatgcagcgg cttg

24

<210> 240

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 240
ttggcagctt catggagg 18

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 241
cctgggcaaa aatgcaac 18

<210> 242
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 242
ctccagctcc tggcgacacct cctc 24

<210> 243
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 243
ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg 45

<210> 244
<211> 3679
<212> DNA
<213> Homo Sapien

<400> 244
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cacacataca cttccctctc cttcactgaa gactcacagt cactcactct 200
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aataaaaaata aataataaca ataaaaaaaa 3679

<210> 245
<211> 713
<212> PRT
<213> Homo Sapien

<400> 245
 Met Arg Leu Leu Val Ala Pro Leu Leu Leu Ala Trp Val Ala Gly
 1 5 10 15
 Ala Thr Ala Thr Val Pro Val Val Pro Trp His Val Pro Cys Pro
 20 25 30
 Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser
 35 40 45
 Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu
 50 55 60
 Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu
 65 70 75
 Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly
 80 85 90
 Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe
 95 100 105
 Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu
 110 115 120
 Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His
 125 130 135
 Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His
 140 145 150

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser
155 160 165

Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile
170 175 180

Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met
185 190 195

Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg
200 205 210

Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu
215 220 225

Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu
230 235 240

Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg
245 250 255

Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys
260 265 270

Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu
275 280 285

His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser
290 295 300

Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu
305 310 315

Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala
320 325 330

Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn
335 340 345

Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn
350 355 360

Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys
365 370 375

Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile
380 385 390

Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg
395 400 405

Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys
410 415 420

Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val
425 430 435

Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu
440 445 450

Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu
455 460 465

Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly
470 475 480

Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr
485 490 495

Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val
500 505 510

Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu
515 520 525

Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His
530 535 540

Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn
545 550 555

Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr
560 565 570

Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr
575 580 585

Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala
590 595 600

Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr
605 610 615

Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly
620 625 630

Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly
635 640 645

Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly
650 655 660

Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser
665 670 675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
680 685 690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu
695 700 705

Leu Pro Pro Leu Ser Gln Asn Ser
710

<210> 246
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 246
aacaaggtaa gatgccatcc tg 22

<210> 247
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 247
aaacttgcg atggagacca gctc 24

<210> 248
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 248
aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249
<211> 3401
<212> DNA
<213> Homo Sapien

<400> 249
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agactcggtc acagtatcaa ataaaatcta taacagaaaa aaaaaaaaaa 3400
a 3401

<210> 250

<211> 546
<212> PRT
<213> Homo Sapien

<400> 250

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Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
			20						25					30
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
			35						40					45
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
			50						55					60
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
			65						70					75
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
			80						85					90
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys
			95						100					105
Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro
			110						115					120
Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu
			125						130					135
Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp
			140						145					150
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu
			155						160					165
Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp
			170						175					180
Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val
			185						190					195
Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu
			200						205					210
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala
			215						220					225

Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp
230 235 240

Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu
245 250 255

Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr
260 265 270

Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu
275 280 285

Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp
290 295 300

Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr
305 310 315

Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr
320 325 330

Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser
335 340 345

Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn
350 355 360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His
365 370 375

Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile
380 385 390

Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu
395 400 405

Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys
410 415 420

Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe
425 430 435

Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala
440 445 450

Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln
455 460 465

Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln
470 475 480

Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile
485 490 495

Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly

500 505 510

Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp
515 520 525

Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg
530 535 540

Ala Asp Lys Glu Gln Ala
545

<210> 251
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 251
caacaatgag ggcaccaagc 20

<210> 252
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 252
gatggctagg ttctggaggt tctg 24

<210> 253
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 253
caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254
<211> 1650
<212> DNA
<213> Homo Sapien

<400> 254
gcctgttgc tgcgtgcgg tgccgtactt gtcatggagc tggcactgcg 50
gcgctctccc gtcccgccgt ggttgctgct gctgccgctg ctgctgggcc 100
tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200

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taaaaaattt atttgtttt atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu
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Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp
20 25 30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val
35 40 45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn
50 55 60

Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
65 70 75

Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu
80 85 90

Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp
95 100 105

Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr
110 115 120

Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu
125 130 135

Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
140 145 150

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
155 160 165

Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
170 175 180

Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
185 190 195

Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
200 205 210

Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
215 220 225

Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
230 235 240

Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys

245	250	255
Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr		
260	265	270
Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser		
275	280	285
Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His		
290	295	300
Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly		
305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln		
440	445	450

Gln Glu

<210> 256
 <211> 1100
 <212> DNA
 <213> Homo Sapien

<400> 256
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 ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
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ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257
<211> 314
<212> PRT
<213> Homo Sapien

<400> 257
Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Ala Arg
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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser
20 25 30
Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
35 40 45
Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
50 55 60
Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
65 70 75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
80									85					90
Ser	Asp	Pro	Ser	Gly	Trp	Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser
95									100					105
Met	Pro	Ser	Phe	Trp	Ser	Leu	Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe
110									115					120
Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	Tyr	Leu	Gly	Asn	Ser	Pro
125									130					135
Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	Val	Thr	Tyr	Thr
140									145					150
Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	Phe	Glu	Phe
155									160					165
Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Ile	Lys
170									175					180
Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	Gln
185									190					195
Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe	Leu	Lys
200									205					210
Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala	Gly
215									220					225
Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly
230									235					240
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val
245									250					255
Val	Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val
260									265					270
Tyr	Thr	Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met
275									280					285
Ala	Gln	Ser	Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu
290									295					300
Phe	Phe	Pro	Leu	Leu	Trp	Ala	Leu	Pro	Leu	Leu	Gly	Pro	Val	
305									310					

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

cccacgcgtc cgccggacgcg tgggaagggc agaatggac tccaaggctg 50

cctcctaggg ctcttgccc tcatcctctc tggcaaatgc agttacagcc 100
cgagccccga ccagcggagg acgctgcccc caggctgggt gtcctggc 150
cgtgcggacc ctgaggaaga gctgagtctc accttgccc tgagacagca 200
gaatgtggaa agactctcg agctggtgca ggctgtgtcg gatcccagct 250
ctcctaata cgaaaatac ctgaccctag agaatgtggc tgatctggtg 300
aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350
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ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagttcat 450
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atcataactca ggtctcccta ctcctgcctt agattcctca ataagatgct 1950
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ccttacttag cttccaggc ttaacttctc tgactactct tgtcttcctc 2250
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tgttagattt tgctcttctc agtttactca ttgtccctg gaacaaatca 2350
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aatgattgat acctcaaata 2427

<210> 259
<211> 556
<212> PRT
<213> Homo Sapien

<400> 259

Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu
1 5 10 15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr
20 25 30

Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu
35 40 45

Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg
50 55 60

Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln
65 70 75

Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg
80 85 90

Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala
95 100 105

Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu
110 115 120

Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly
125 130 135

Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val
140 145 150

Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro
155 160 165

His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser
170 175 180

Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly
185 190 195

Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn
200 205 210

Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln
215 220 225

Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu
230 235 240

Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala
245 250 255

Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly
260 265 270

Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala
275 280 285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly
290 295 300

Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser
305 310 315

Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp
320 325 330

Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met
335 340 345

Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp
350 355 360

Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg
365 370 375

Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly
380 385 390

Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp
395 400 405

Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser
410 415 420

Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His
425 430 435

Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro
440 445 450

Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg
455 460 465

Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val
470 475 480

Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser
485 490 495

Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln
500 505 510

His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser
515 520 525

Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro
530 535 540

Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu
545 550 555

Cys

<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien

<400> 260
gccgcgcgct ctctccggc gcccacacct gtctgagcgg cgcagcggc 50
cgcgccccgg gcgggctgct cggcgccgaa cagtgcgtgg catggcaggg 100
attccagggc tcctcttcct tctttcttt ctgctctgtg ctgttggca 150
agtgagccct tacagtgccc cctggaaacc cacttggcct gcataccgcc 200

tccctgtcg tttgtccccag tctaccctca atttagccaa gccagactt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300
taagggact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcac 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttcctgctca actacccttt ctcaacatca 550
gtgaagttat ccacgggctg caccggcacc ctggggcag agaagcatgt 600
cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttcctaaagc ccaagttaa agatggtggt 700
cgaggggcca acgactccac ttcagccatg cccgagcaga taaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaaggcga 800
atgccaatga catcggcatg gattatgatt atgccttcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctccctgctaa 900
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
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ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150
gatttcaacg tggctgtcag aatcactcct ctcaaataatg cccagattt 1200
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ttccctcctg gcagcaatta agggcttca tgttcttatt ttaggagagg 1300
ccaaattgtt ttttgcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgt 1350
tgtgtgttaag gtgtcttata atctttacc tatttcttac aattgcaaga 1400
tgactggctt tactatttga aaactggttt gtgtatcata tcataatatca 1450
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tttggggcaa tgaggaatat ttgacaatata agttaatctt cacgttttg 1550
caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600

atatttggca tacaagagat atgaaaaaaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu
1 5 10 15

Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro
20 25 30

Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr
35 40 45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu
50 55 60

Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu
65 70 75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu
80 85 90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile
95 100 105

Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser
110 115 120

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
125 130 135

Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
140 145 150

Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
155 160 165

Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
170 175 180

Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
185 190 195

Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
200 205 210

Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
215 220 225

Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
230 235 240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
245 250 255

His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
260 265 270

Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
275 280 285

Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
290 295 300

Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
305 310 315

Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
320 325 330

Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
335 340 345

Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
350 355 360

Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
365 370 375

Asn Tyr Leu Asp Cys Arg Glu Gly
380

<210> 262
<211> 1378
<212> DNA
<213> Homo Sapien

<400> 262
gcatcgccct gggtctctcg agcctgctgc ctgctcccc gccccaccag 50
ccatgggtgt ttctggagcg ccccccagccc tgggtggggg ctgtctcg 100
actttcaccc ctctgctgct gctggcgctcg acagccatcc tcaatgcggc 150
caggataacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200
ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
atccagaaga atgggaccca ccactgcgca gtttctctgc tcaccagccg 300
ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
cgtcccaaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450
ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500
ccatacagtt ctcagagcgg gtcctgcccc tctgcctacc tgatgcctct 550

atccacacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600
ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650
ttccttatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700
ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750
ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850
gccgagcgca acaggccccgg ggtctacatc agcctctctg cgcaccgctc 900
ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950
ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000
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ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350
ataaaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
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Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
					20				25				30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
					35				40				45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
					50			55					60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
					65			70					75	

Ala Gly Ser Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His
80 85 90

Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu
95 100 105

Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys
110 115 120

Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys
125 130 135

Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser
140 145 150

Ile Gln Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala
155 160 165

Ser Ile His Leu Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp
170 175 180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
185 190 195

Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
200 205 210

Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
215 220 225

Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
230 235 240

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
245 250 255

Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
260 265 270

Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
275 280 285

Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
290 295 300

Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
305 310 315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264
gtccgcaagg atgcctacat gttc 24

<210> 265
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 265
gcagaggtgt ctaaggttg 19

<210> 266
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa ctttcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 268
gggaaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269

gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatggac tccaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agcccgagc ccgac 45

<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
ggcagggat tccagggctc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgcatt gctggtagag caag 24

<210> 280

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 280
ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gtcataaca gttcccttgc cccca 34

<210> 282
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 282
tggaggggga gcgggatgct tgtctggcg actccgggg cccccctcatg 50
tgccaggtgg a 61

<210> 283
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 283
ccctcagacc ctgcagaagc tgaagggttcc tatcatcgac tcggaagtct 50
gcagccatct gtactggcg ggagcaggac agggaccat cactgaggac 100
atgctgtgtg ccggctact 119

<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien

<400> 284
gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggc ggccaccaca ggccccgtt gaggccctcac 100
agatgaggag aaacgtttga tgggtggagct gcacaacctc taccgggccc 150
aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250
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aatgggtact cttttccc tagcaacggg gattccggct ttcttggtaa 750
cagaggtctc aggctccctg gcaaccaagg ctctgcctgc tgtggaaacc 800
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<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met His Gly Ser Cys Ser Phe Leu Met Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp
20 25 30

Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala
35 40 45

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp
50 55 60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val
65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe
80 85 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu
95 100 105

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys
110 115 120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala
125 130 135

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
140 145 150

Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
155 160 165

Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly

170	175	180
Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser		
185	190	195
Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro		
200	205	210
Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser		
215	220	225
Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile		
230	235	240
Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys		
245	250	255
Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr		
260	265	270
Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr		
275	280	285
Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu		
290	295	300
Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile		
305	310	315
Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser		
320	325	330
Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly		
335	340	345
Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu		
350	355	360
Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro		
365	370	375
Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr		
380	385	390
Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser		
395	400	405
Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser		
410	415	420
Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser		
425	430	435
Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly		
440	445	450
Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe		

455

460

<210> 286
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 286
tcctgcagtt tcctgatgc 19

<210> 287
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 287
ctcatattgc acaccagtaa ttcg 24

<210> 288
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 288
atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289
<211> 3662
<212> DNA
<213> Homo Sapien

<400> 289
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caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaactga 200
acaacaatga attggagacc attccaaatc tgggaccagt ctcggcaaat 250
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acatctgaaa gagtttcagt cccttggaaac tttggacctt agcagcaaca 350
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tatctcaaca gcaaccgagt cacatcaatg gaacctgggt atttgacaa 450
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gaaaatgagt tactaaagca ttttaataa tacctgcctt gtaccattt 3600
ttaaatagaa gttacttcat tatatttgc acattatatt taataaaatg 3650
tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met Val Asp Val Leu Leu Leu Phe Ser Leu Cys Leu Leu Phe His
1 5 10 15

Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
20 25 30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
35 40 45

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
50 55 60

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
65 70 75

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
80 85 90

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
95 100 105

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
110 115 120

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
125 130 135

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
140 145 150

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

155 160 165

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
170 175 180

Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
185 190 195

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
200 205 210

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
215 220 225

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
230 235 240

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
245 250 255

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
260 265 270

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
275 280 285

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser
290 295 300

Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile
305 310 315

Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg
320 325 330

Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala
335 340 345

Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn
350 355 360

Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys
365 370 375

Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys
380 385 390

Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln
395 400 405

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly
410 415 420

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
425 430 435

Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala
440 445 450

Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
455 460 465

Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu
470 475 480

Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
485 490 495

Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
500 505 510

Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
515 520 525

His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
530 535 540

Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
545 550 555

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
560 565 570

Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
575 580 585

Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
590 595 600

Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
605 610 615

Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
620 625 630

Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
635 640 645

Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
650 655 660

Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
665 670 675

Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
680 685 690

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
695 700 705

Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
710 715 720

Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met

725	730	735
Thr Ala Pro Ser Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly Val	
740	745	750
Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val		
755	760	765
Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys		
770	775	780
Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro		
785	790	795
Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly		
800	805	810
Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser		
815	820	825
Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr		
830	835	840
Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr		
845	850	855
Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr		
860	865	870
Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His		
875	880	885
Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr		
890	895	900
Glu Pro Ser Tyr Ile Lys Lys Glu Cys Tyr Pro Cys Ser His		
905	910	915
Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp		
920	925	930
Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn		
935	940	945
Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu		
950	955	960
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
965	970	975
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
980	985	990
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
995	1000	1005

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
1010 1015 1020
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
1025 1030 1035
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
1040 1045 1050
Asn Phe Gln Ser Tyr Asp Leu Asp Thr
1055

<210> 291
<211> 2906
<212> DNA
<213> Homo Sapien

<400> 291
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ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agcttctcc 100
tggAACCGAA cgcaatggat aaactgattt tgcaagagag aaggaagaac 150
gaagctttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
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caaaaa 2906

<210> 292
<211> 640
<212> PRT
<213> Homo Sapien

<400> 292

Met Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly
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Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu
20 25 30

Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
35 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser
155 160 165

Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly
170 175 180

Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly
185 190 195

Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg
200 205 210

Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp
215 220 225

Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln
230 235 240

Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile
245 250 255

Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val
260 265 270

Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp
275 280 285

Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His
290 295 300

Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp
305 310 315

Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys
320 325 330

Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp
335 340 345

Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro
350 355 360

Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys
365 370 375

Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn
380 385 390

Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val
395 400 405

Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp
410 415 420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
425 430 435

Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
440 445 450

Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
455 460 465

Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
470 475 480

Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
485 490 495

Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
500 505 510

Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
515 520 525

Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
530 535 540

Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
545 550 555

Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
560 565 570

Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
575 580 585

Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
590 595 600

Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn
605 610 615

Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn
620 625 630

Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
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<210> 293
<211> 4053
<212> DNA

<213> Homo Sapien

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aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150
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aaa 4053

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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
215 220 225

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
230 235 240

Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
245 250 255

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
260 265 270

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
275 280 285

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
290 295 300

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
305 310 315

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
320 325 330

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
335 340 345

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser
350 355 360

Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile
365 370 375

Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg
380 385 390

Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala
395 400 405

Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn
410 415 420

Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys
425 430 435

Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys
440 445 450

Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln
455 460 465

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly
470 475 480

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
485 490 495

Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala
500 505 510

Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
515 520 525

Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu
530 535 540

Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
545 550 555

Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
560 565 570

Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
575 580 585

His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
590 595 600

Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
605 610 615

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
620 625 630

Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
635 640 645

Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
650 655 660

Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
665 670 675

Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
680 685 690

Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
695 700 705

Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
710 715 720

Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
725 730 735

Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
740 745 750

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
755 760 765

Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
770 775 780

Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
785 790 795

Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
800 805 810

Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
815 820 825

Trp Val Val Ile Ile Tyr His Thr Arg Arg Asn Glu Asp Cys
830 835 840

Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
845 850 855

Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
860 865 870

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
875 880 885

Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
890 895 900

Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
905 910 915

Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
920 925 930

Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
935 940 945

Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
950 955 960

Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
965 970 975

Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
980 985 990

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
995 1000 1005

Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
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Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
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Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
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Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
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Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
1070 1075 1080

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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Asn Phe Gln Ser Tyr Asp Leu Asp Thr
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<212> DNA
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<220>
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<400> 296
cctaaactga actggacca 19

<210> 297
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<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 297
ggctggagac actgaacct 19

<210> 298
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acagctgcac agctcagaac agtg 24

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<400> 299
cattcccaagt ataaaaattt tc 22

<210> 300
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<223> Synthetic Oligonucleotide Probe

<400> 300
gggtcttggt gaatgagg 18

<210> 301

<211> 24
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gtgcctctcg gttaccacca atgg 24

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<210> 309
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<212> DNA
<213> Homo Sapien

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<210> 311
<211> 22
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 311
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<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 312
gcggccacgg tccttgaaa tg 22

<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 313
tgaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314
<211> 3003
<212> DNA
<213> Homo Sapien

<400> 314
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cgccgctgtc ctccggagc ggcagcagta gcccggcgg cgagggctgg 100
gggttcctcg agactctcag agggggcgct cccatcgccg cccaccaccc 150
caacctgttc ctcgcgcgcc actgcgctgc gccccaggac ccgctgcccc 200

acatggatt tctccctggcg ctgggtgctgg tattcctcgct ctacacctgcag 250
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tggcctatgt cgttatggtg ggaggattga ctgctgctgg ggctgggctc 350
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aat 3003

<210> 315
<211> 509
<212> PRT
<213> Homo Sapien

<400> 315

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35 40 45

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
50 55 60

Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
65 70 75

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
80 85 90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
95 100 105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
110 115 120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
125 130 135

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
140 145 150

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
155 160 165

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
170 175 180

Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
185 190 195

Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
200 205 210

Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
215 220 225

Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
230 235 240

Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
245 250 255

Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
260 265 270
Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
275 280 285
Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro
290 295 300
Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr
305 310 315
Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro
320 325 330
Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
335 340 345
Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala
350 355 360
Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln
365 370 375
Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val
380 385 390
His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu
395 400 405
Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly
410 415 420
Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys
425 430 435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly
440 445 450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser
455 460 465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala
470 475 480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln
485 490 495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg
500 505

<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 316
gatggttcct gctcaagtgc cctg 24

<210> 317
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 317
ttgcacttgt aggacccacg tacg 24

<210> 318
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 318
ctgatggag gacctgtgta gatgttgcgt aatgtgctac aggaagagcc 50

<210> 319
<211> 2110
<212> DNA
<213> Homo Sapien

<400> 319
ctctttgaa aaggattatc acctgatcag gttctctctg catttgc 50
tttagattgt gaaatgtggc tcaagggtctt cacaacttgc ctttccttg 100
caacaggtgc ttgctcg 150
catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200
cactccagca tcagacatcc agatcatatg gctatttgc 250
caatgcccaa atacttactg ggctctgtga ataagtctgt gttcctgac 300
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aaaaaaaaaa 2110

<210> 320
<211> 450
<212> PRT
<213> Homo Sapien

<400> 320
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Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His
20 25 30
Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
35 40 45
His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
50 55 60
Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
65 70 75
Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
80 85 90
Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
95 100 105
Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
110 115 120
Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
125 130 135
Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
140 145 150
Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
155 160 165
Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
170 175 180
Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
185 190 195
Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
200 205 210
Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
215 220 225

Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
230 235 240

Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
245 250 255

Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
260 265 270

Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
275 280 285

Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
290 295 300

Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
305 310 315

Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu
320 325 330

Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly
335 340 345

Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp
350 355 360

Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly
365 370 375

Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His
380 385 390

Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe
395 400 405

Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro
410 415 420

Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr
425 430 435

Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu
440 445 450

<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatcctgtca caaaggccagt ggtgc 25

<210> 322
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 322
cactgacagg gttcctcacc cagg 24

<210> 323
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 323
ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324
<211> 2397
<212> DNA
<213> Homo Sapien

<400> 324
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acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150
tggatgatag aattttatgc cccgtggtgc cctgcttgc aaaatcttca 200
accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250
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aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaaaa 2397

<210> 325
<211> 280
<212> PRT

<213> Homo Sapien

<400> 325
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Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn
20 25 30
Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly
35 40 45
Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
50 55 60
Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75
Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
80 85 90
Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
95 100 105
Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
110 115 120
Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
125 130 135
Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
140 145 150
Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
155 160 165
His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
170 175 180
Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu
215 220 225

Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
245 250 255

Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
260 265 270

Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
275 280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

tgaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 330
ggagtcttgc agttcccttg gcagtcctgg tgctgttgct ttggg 45

<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

<400> 331
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<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

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Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
	20					25								30
Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys
	35						40							45
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
	50						55							60
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
	65						70							75
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
	80						85							90
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
	95						100							105
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
	110						115							120
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
	125						130							135
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
	140						145							150
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
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Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
	170						175							180
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
	185							190						195
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu
	200							205						210
Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Phe	Gln	Leu	Gly	Asp	Leu	His	Arg
	215							220						225
Ala	Leu	Glu	Leu	Thr	Arg	Arg	Leu	Leu	Ser	Leu	Asp	Pro	Ser	His
	230							235						240
Glu	Arg	Ala	Gly	Gly	Asn	Leu	Arg	Tyr	Phe	Glu	Gln	Leu	Leu	Glu
	245							250						255
Glu	Glu	Arg	Glu	Lys	Thr	Leu	Thr	Asn	Gln	Thr	Glu	Ala	Glu	Leu
	260							265						270

Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro
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Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys
290 295 300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His
305 310 315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu
320 325 330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met
335 340 345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys
350 355 360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr
365 370 375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp
380 385 390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile
395 400 405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn
410 415 420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg
425 430 435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala
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455 460 465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr
470 475 480
Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
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Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
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<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333
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<210> 334

<211> 19

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<223> Synthetic Oligonucleotide Probe

<400> 334
ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 335
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<210> 336

<211> 24

<212> DNA

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<223> Synthetic Oligonucleotide Probe

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<210> 337

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<210> 338

<211> 2789

<212> DNA

<213> Homo Sapien

<400> 338

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<210> 339
<211> 772
<212> PRT
<213> Homo Sapien

<400> 339

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Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
		20					25					30		
Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
		35					40					45		
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
		50					55					60		
Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
		65					70					75		
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
		80					85					90		
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
		95					100					105		
Val	Leu	Thr	Ser	Arg	Ala	Thr	Leu	Ser	Thr	Leu	Ala	Val	Ala	Val
		110					115					120		
Asn	Arg	Thr	Val	Ala	His	His	Phe	Pro	Arg	Leu	Leu	Tyr	Phe	Thr
		125					130					135		
Gly	Gln	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Gly	Met	Gln	Val	Val	Ser
		140					145					150		
His	Gly	Asp	Glu	Arg	Pro	Ala	Trp	Leu	Met	Ser	Glu	Thr	Leu	Arg
		155					160					165		
His	Leu	His	Thr	His	Phe	Gly	Ala	Asp	Tyr	Asp	Trp	Phe	Phe	Ile
		170					175					180		
Met	Gln	Asp	Asp	Thr	Tyr	Val	Gln	Ala	Pro	Arg	Leu	Ala	Ala	Leu
		185					190					195		
Ala	Gly	His	Leu	Ser	Ile	Asn	Gln	Asp	Leu	Tyr	Leu	Gly	Arg	Ala
		200					205					210		
Glu	Glu	Phe	Ile	Gly	Ala	Gly	Glu	Gln	Ala	Arg	Tyr	Cys	His	Gly
		215					220					225		
Gly	Phe	Gly	Tyr	Leu	Leu	Ser	Arg	Ser	Leu	Leu	Leu	Arg	Leu	Arg
		230					235					240		
Pro	His	Leu	Asp	Gly	Cys	Arg	Gly	Asp	Ile	Leu	Ser	Ala	Arg	Pro
		245					250					255		

Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly
260 265 270

Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu
275 280 285

Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu
290 295 300

Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr
305 310 315

Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr
320 325 330

Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val
335 340 345

Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu
350 355 360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp
365 370 375

Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala
380 385 390

Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp
395 400 405

Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro
410 415 420

Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg
425 430 435

Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu
440 445 450

Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg
455 460 465

Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met
470 475 480

Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu
485 490 495

Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe
500 505 510

Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
515 520 525

Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
530 535 540

Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg
545 550 555

Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
560 565 570

Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
575 580 585

Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
590 595 600

Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
605 610 615

Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
635 640 645

Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
650 655 660

Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
665 670 675

Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
680 685 690

Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
695 700 705

Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
710 715 720

Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
725 730 735

Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
740 745 750

Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
755 760 765

Gln Glu Gln Ala Asn Ser Thr
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<210> 340
<211> 1572
<212> DNA
<213> Homo Sapien

<400> 340
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cttttgaag ggtgtatgc ttgaaagcat tttctgtgct ttgatcacta 150
tgcttagaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
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attnaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

<400> 341

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Gly His Gly Asn Arg Met His His His Glu His His His Leu Gln
35 40 45

Ala Pro Asn Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg
50 55 60

Met Glu Leu Ser Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val
65 70 75

Lys Pro Lys Asp Val Ser Leu Trp Ala Ala Val Lys Glu Thr Trp
80 85 90

Thr Lys His Cys Asp Lys Ala Glu Phe Phe Ser Ser Glu Asn Val
95 100 105

Lys Val Phe Glu Ser Ile Asn Met Asp Thr Asn Asp Met Trp Leu
110 115 120

Met Met Arg Lys Ala Tyr Lys Tyr Ala Phe Asp Lys Tyr Arg Asp
125 130 135

Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr Thr Phe Ala Ile
140 145 150

Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp Pro Ser Gln
155 160 165

Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu Glu Tyr
170 175 180

Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met Lys
185 190 195

Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln
200 205 210

Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val
215 220 225

Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala
230 235 240

Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile
245 250 255

Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys
260 265 270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly
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His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser
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Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 342

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<210> 343

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<212> DNA

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<211> 28

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<400> 344

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<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

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<400> 345
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<400> 347
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<210> 348
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<400> 348
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<400> 349
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<210> 351
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<220>
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<400> 351
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<210> 352
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<210> 354
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<400> 355

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<400> 356
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<210> 357
<211> 48
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<400> 357
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<210> 358
<211> 47
<212> DNA
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<400> 358
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<210> 359
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<400> 359
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<210> 360
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<210> 365
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<210> 366
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<212> DNA
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<210> 367
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<212> DNA
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<400> 367
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<210> 368
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<400> 368
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<210> 369
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<400> 369
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<210> 370
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<210> 371
<211> 48
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<213> Artificial Sequence

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<400> 371
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<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373
ctatgaaatt aaccctcaact aaagggagta agggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374
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<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

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aaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150
tgcttcttccc cccaaatgtt cttatggact gttgctggta tccccatcct 200
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gagagactct tcaaacccaa ggcaaaatttgaatgttca acctgtttcc 700
tcaattattt tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750
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agagcaagaa catggccaca cccaccgccc cacacgagaa atttgcgc 850
tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900
taagtagttt taaatgtttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 997

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<212> PRT
<213> Homo Sapien

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Cys Phe Ser Ser Gln Met Phe Leu Trp Thr Val Ala Gly Ile Pro
20 25 30
Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr
35 40 45
Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro

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Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser		
65	70	75
Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser		
80	85	90
Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu		
95	100	105
Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser		
110	115	120
Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg		
125	130	135
Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp		
140	145	150
Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp		
155	160	165
Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala		
170	175	180
Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val		
185	190	195
Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile		
200	205	210
Asn Pro Leu Asn Lys Gly Lys Ser Leu		
215		

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

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<210> 379

<211> 24

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<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380
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<210> 381
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<220>
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<400> 381
gcagattttg aggacagcca cctcca 26

<210> 382
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<220>
<223> Synthetic oligonucleotide probe

<400> 382
ggccttgcag acaaccgt 18

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<210> 384
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<220>
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<400> 384
cagctgccct tccccaaacca 20

<210> 385
<211> 18

<212> DNA
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<220>
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<400> 385
catcaagcgc ctctacca 18

<210> 386
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<220>
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<400> 386
cacaaactcg aactgcttct g 21

<210> 387
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<220>
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<400> 387
gggccatcac agctccct 18

<210> 388
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<400> 388
gggatgtggc gaacacagaa ca 22

<210> 389
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<400> 389
tgccagctgc atgctgccag tt 22

<210> 390
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<400> 390
cagaaggatg tcccgtaaa 20

<210> 391

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<400> 391
gccgctgtcc actgcag 17

<210> 392

<211> 21

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<400> 392
gacggcatcc tcagggccac a 21

<210> 393

<211> 20

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 393
atgtcctcca tgcccacgca 20

<210> 394

<211> 20

<212> DNA

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<400> 394
gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

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<213> Artificial Sequence

<220>
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<400> 395
ccgcagcctc agtgatga 18

<210> 396
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<400> 396
gaagagcaca gctgcagatc c 21

<210> 397
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<400> 397
gaggtgtcct ggctttggta gt 22

<210> 398
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<400> 398
cctctggcgc ccccactcaa 20

<210> 399
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<400> 399
ccaggagagc tggcgatg 18

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<400> 400
gcaaattcag ggctcactag aga 23

<210> 401
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cacagagcat ttgtccatca gcagttcag 29

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<400> 402
ggcagagact tccagtcact ga 22

<210> 403
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<400> 403
gccaagggtg gtgttagata gg 22

<210> 404
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<220>
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<400> 404
caggccccct tgatctgtac ccca 24

<210> 405
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<400> 405

gggacgtgct tctacaagaa cag 23
<210> 406
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<220>
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<400> 406
caggcttaca atgttatgtat cagaca 26

<210> 407
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<400> 407
tattcagagt tttccattgg cagtgccagt t 31

<210> 408
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<210> 409
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cgatcttctc cacccaggag cg 23

<210> 410
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<400> 410
gccaggcctc acattcgt 18

<210> 411
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<400> 411
ctccctgaat ggcagcctga gca 23

<210> 412
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<212> DNA
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<400> 412
aggtgtttat taagggccta cgct 24

<210> 413
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<400> 413
cagagcagag ggtgccttg 19

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<400> 414
tggcggagtc ccctcttggc t 21

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<400> 416
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<210> 417
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<400> 419
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<400> 420
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<400> 421

tctgtccacc atcttgcctt g 21

<210> 422

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<212> DNA

<213> Homo Sapien

<400> 422

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atggcgctga ggcggccacc gcgactccgg ctctgcgcgc ggctgcctga 100

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tcaaatccag caatcgaacc ccagtggcac aggaatttga aagtgtggaa 200

ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250

gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300

ttcagggaga cttggcggtt cgtgcagaaa tactggggaa gacatccctg 350

aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400

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<212> PRT
<213> Homo Sapien

<400> 423
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Pro Asp Phe Phe Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly
20 25 30

Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu

35	40	45
Phe Glu Ser Val Glu Leu Ser Cys Ile Ile	Thr Asp Ser Gln Thr	
50	55	60
Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile	Gln Asp Glu Gln Thr	
65	70	75
Thr Tyr Val Phe Phe Asn Lys Ile Gln Gly	Asp Leu Ala Gly	
80	85	90
Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu	Lys Ile Trp Asn Val	
95	100	105
Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys	Glu Val Val Ala Arg	
110	115	120
Asn Asp Arg Lys Glu Ile Asp Glu Ile Val	Ile Glu Leu Thr Val	
125	130	135
Gln Val Lys Pro Val Thr Pro Val Cys Arg	Val Pro Lys Ala Val	
140	145	150
Pro Val Gly Lys Met Ala Thr Leu His Cys	Gln Glu Ser Glu Gly	
155	160	165
His Pro Arg Pro His Tyr Ser Trp Tyr Arg	Asn Asp Val Pro Leu	
170	175	180
Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe	Arg Asn Ser Ser Phe	
185	190	195
His Leu Asn Ser Glu Thr Gly Thr Leu Val	Phe Thr Ala Val His	
200	205	210
Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile	Ala Ser Asn Asp Ala	
215	220	225
Gly Ser Ala Arg Cys Glu Glu Gln Glu Met	Glu Val Tyr Asp Leu	
230	235	240
Asn Ile Gly Gly Ile Ile Gly Gly Val Leu	Val Val Leu Ala Val	
245	250	255
Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys	Ala Tyr Arg Arg Gly	
260	265	270
Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu	Ser Tyr Lys Asn Pro	
275	280	285
Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg	Thr Asp Glu Glu Gly	
290	295	300
Asp Phe Arg His Lys Ser Ser Phe Val Ile		
305	310	